

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 04:16:53 ; Search time 209 Seconds
(without alignments)
1002.085 Million cell updates/sec

Title: US-09-843-377-3_COPY_1000_1092

Perfect score: 93
Sequence: 1 gagctgggagacatccatcc.....ctccagaaacattgagtg 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	19.4	43 22 AAC90373	pFlag-OMV-5a:METH1
2	17	18.3	32 9 AAN80618	Probe (32n) for th
3	17	18.3	49 24 AAI45727	Cancer cells detec
4	16.8	18.1	50 22 AAI75541	Human silent SNP c
5	16.6	17.8	30 20 AAX07403	Oncorhynchus nerka
6	16.6	17.8	33 21 AAC64543	Herpesvirus expres
7	16.6	17.8	39 16 AAT08201	Amplification prim
8	16.6	17.8	43 22 AAC90375	pC4FC:METH1 PCR pr
9	16.6	17.8	47 21 AAZ66265	Human map-related

10	16.6	17.8	50 15 AAG63029	Primer used in SEL
11	16.6	17.8	50 16 AAG98309	SPRex primer 1 mol
12	16.6	17.8	50 22 AAL29115	Human SNP oligonuc
13	16.6	17.8	50 22 AAF70543	STEX experiment o
14	16.4	17.6	47 19 AAV29852	5' VH primer for e
15	16.4	17.6	47 21 AA67105	Human map-related
16	16.4	17.6	50 22 AAL34180	Human SNP oligonuc
17	16.4	17.6	50 22 AAT75539	Human silent SNP c
18	16.2	17.4	40 18 AAT98491	Template switching
19	16.2	17.4	40 20 AAZ28729	Oligonucleotide Na
20	16.2	17.4	50 18 AAT76941	Staphylococcus aur
21	16.2	17.4	50 22 AAL27838	Human SNP oligonuc
22	16.2	17.4	50 22 AAL34304	Human SNP oligonuc
23	16.2	17.2	41 22 AAI64807	Staphylococcus
24	16.2	17.2	43 21 AAZ9817	Cis-acting nucleot
25	16.2	17.2	50 21 AAZ9815	Sequence of the st
26	16.2	17.2	50 22 AAT33971	Human SNP oligonuc
27	16.2	17.2	50 22 AAT89751	Human coding sequ
28	15.8	17.0	35 20 AAV63698	PCR primer used to
29	15.8	17.0	39 20 AAT28217	Mouse splice accep
30	15.8	17.0	39 21 AAZ9286	Splice acceptor se
31	15.8	17.0	40 20 AAX89506	Sequence of primer
32	15.8	17.0	44 15 AAG65503	Transketolase gene
33	15.8	17.0	44 24 AAL43960	Polynucleotide sep
34	15.8	17.0	46 20 AAZ26503	WO 9909191 Segid #
35	15.8	17.0	47 21 AAT67047	Human map-related
36	15.8	17.0	48 21 AAX9938	Oligonucleotide p1
37	15.8	17.0	48 21 AAC58575	Human DNA4374 43
38	15.6	16.8	27 22 AAK52192	Human Oshbeta14 CD
39	15.6	16.8	30 24 ABR52162	Mouse N-calcium ch
40	15.6	16.8	31 22 AAL30206	Human single nucle
41	15.6	16.8	33 24 ABL41371	Human transcriptio
42	15.6	16.8	35 20 AAZ07103	Recombinant PC gen
43	15.6	16.8	43 20 AAY99100	DNA methyltransfer
44	15.6	16.8	47 21 AAZ68364	Human map-related
45	15.6	16.8	50 22 AAT73671	Human silent SNP c
46	15.6	16.8	50 22 AAT86692	Human G-protein su
47	15.6	16.8	50 22 AAB48693	Human G-protein su
48	15.6	16.8	28 24 ABL50681	Rat G-protein-coupl
49	15.4	16.6	30 21 AAZ88883	Human wolframin in
50	15.4	16.6	31 16 AAT04205	PCR primer oligo B
51	15.4	16.6	31 19 AAV11384	Potato matrix proc
52	15.4	16.6	31 19 AAV10420	Potato MPP PCR pri
53	15.4	16.6	39 22 AAT89684	Probe used to iden
54	15.4	16.6	41 18 AAT65388	Human keratinocyte
55	15.4	16.6	41 19 AAV51124	Maize polymorphic
56	15.4	16.6	41 19 AAV51123	Maize polymorphic
57	15.4	16.6	44 22 AAT60319	Cap independent tr
58	15.4	16.6	47 21 AAZ68249	Human map-related
59	15.2	16.3	29 20 AAZ19908	Human foetal kidn
60	15.2	16.3	29 21 AAT01570	Hammerhead ribozym
61	15.2	16.3	33 24 AAS17330	Overlapping primer
62	15.2	16.3	36 19 AAV6536	PCR primer for ser
63	15.2	16.3	36 21 AAC64550	Herpesvirus expres
64	15.2	16.3	36 22 AAT68432	M. organophilum me
65	15.2	16.3	41 19 AAV50773	Brassica sp. polym
66	15.2	16.3	41 24 ABL96120	Brassica polymorph
67	15.2	16.3	46 20 AAX90642	Primer FIV9 to gen
68	15.2	16.3	46 20 ABL60729	Packaging expressi
69	15.2	16.3	47 21 AAZ66988	Human map-related
70	15.2	16.3	48 20 AAZ23367	Plasmid pI-AN7 DNA
71	15.2	16.3	50 16 AAG99206	Human HPR1 gene pr
72	15.2	16.3	15 24 ABR88813	Adaptor oligonucle
73	15.2	16.3	15 24 ABR12602	Topoisomerase adap
74	15.2	16.3	16 20 AAZ25796	Expression plasmid
75	15.2	16.3	29 24 ABR69427	PCR primer OGR48 f
76	15.2	16.3	33 24 AAL42596	Human dynein recep
77	15.2	16.3	36 20 AAX89909	Sequence of primer
78	15.2	16.3	36 20 AAX89910	Sequence of primer
79	15.2	16.3	41 16 AAG99700	Bovine respiratory
80	15.2	16.3	41 16 AAG97660	Bovine respiratory
81	15.2	16.3	41 16 AAV47871	Maize polymorphic
82	15.2	16.3	41 19 AAV47872	Maize polymorphic

C	83	15	16.1	41	19	AAV26221	BRV strain 375 (V	C	156	14.6	15.7	50	22	AAI33945	Human SNP oligonuc
C	84	15	16.1	41	21	AAV37500	Reest acyltransfer	C	157	14.4	15.5	17	16	AAQ95462	Primer B (Group 3,
C	85	15	16.1	41	24	AAV4539	12C45 epitope DNA	C	158	14.4	15.5	19	19	AAV35420	C. histolyticum CH
C	86	15	16.1	42	18	AAV6570	Primer used in MHC	C	159	14.4	15.5	20	14	AAO50576	Asparaginylendopep
C	87	15	16.1	43	18	AAV74319	Construct pcGNN-ZF	C	160	14.4	15.5	20	20	AAZ21785	Exemplary oligonuc
C	88	15	16.1	45	19	AAV03898	Primer MP16 for ch	C	161	14.4	15.5	20	24	ABK51668	Human ABCG5 gene P
C	89	15	16.1	45	22	AAH46988	PCR mutagenic prim	C	162	14.4	15.5	24	22	AAH76860	Human tyrosinase 1
C	90	15	16.1	47	21	AAZ62554	Human map-related	C	163	14.4	15.5	24	24	ABO00576	Oligonucleotide ad
C	91	15	16.1	48	20	AAH82220	Influenza virus H7	C	164	14.4	15.5	24	24	ABO00589	Oligonucleotide ad
C	92	15	16.1	50	22	AAI75840	Human silent SNP c	C	165	14.4	15.5	24	24	ABO05130	Oligonucleotide ad
C	93	14.8	15.9	19	21	AAI26628	Human HPC1 mutatio	C	166	14.4	15.5	24	24	ABO11417	Oligonucleotide ad
C	94	14.8	15.9	21	24	AAI72913	Interleukin 18 (IL	C	167	14.4	15.5	24	24	ABO11417	Oligonucleotide ad
C	95	14.8	15.9	27	18	AAI72318	Mouse ILK-1 VEGF r	C	168	14.4	15.5	25	24	ABO11458	Oligonucleotide ad
C	96	14.8	15.9	27	18	AAI70909	Human KKR VEGF rec	C	169	14.4	15.5	25	24	ABO12953	Oligonucleotide ad
C	97	14.8	15.9	30	20	AAZ07913	Primer for celllobl	C	170	14.4	15.5	25	24	ABO12994	Oligonucleotide ad
C	98	14.8	15.9	30	20	AAZ09713	Human Fc-gammaR1a	C	171	14.4	15.5	25	24	ABO12994	Oligonucleotide ad
C	99	14.8	15.9	31	20	AAZ06223	Human biallelic po	C	172	14.4	15.5	26	20	AAH78418	Human GMP1-1 25-m
C	100	14.8	15.9	36	18	AAI60552	Progestin regulate	C	173	14.4	15.5	26	20	AAH78418	Human GMP1-1 25-m
C	101	14.8	15.9	36	24	ABK49926	Beta2M/HFE monoch	C	174	14.4	15.5	26	20	AAH78418	Human GMP1-1 25-m
C	102	14.8	15.9	38	23	AAI21115	T. brucei trypanos	C	175	14.4	15.5	29	18	AAH89082	Interleukin 10 pro
C	103	14.8	15.9	38	23	ABK04860	Human NOG0. Inozyme	C	176	14.4	15.5	29	18	AAH89082	Primer BCD2N. Syn
C	104	14.8	15.9	40	22	AAI83798	Dengue-3 virus der	C	177	14.4	15.5	31	19	AAH89082	Polymorphic fragme
C	105	14.8	15.9	41	24	ABU42406	Human alpha 2,3-si	C	178	14.4	15.5	31	19	AAH89082	Grib-alpha oligonu
C	106	14.8	15.9	41	24	ABU42406	Human IAR protein	C	179	14.4	15.5	31	19	AAH89082	Nucleotide fragmen
C	107	14.8	15.9	44	22	ABH52983	Human LAR protein	C	180	14.4	15.5	31	19	AAH89082	Primer for amplif
C	108	14.8	15.9	44	22	ABH52983	Human LAR protein	C	181	14.4	15.5	31	19	AAH89082	Primer for amplif
C	109	14.8	15.9	45	15	AAH89697	Human transcrip	C	182	14.4	15.5	34	18	AAH89082	Primer for amplif
C	110	14.8	15.9	47	23	AAH8652	Mink growth hormon	C	183	14.4	15.5	34	18	AAH89082	Primer for amplif
C	111	14.8	15.9	48	13	AAH8652	CNS disorder-relat	C	184	14.4	15.5	35	21	AAH89082	Primer for amplif
C	112	14.8	15.9	48	13	AAH8652	Primer Hui55BCKno	C	185	14.4	15.5	35	21	AAH89082	Primer for amplif
C	113	14.8	15.9	50	14	AAH8652	Upstream sequence	C	186	14.4	15.5	37	21	AAH89082	Primer for amplif
C	114	14.8	15.9	50	22	AAI30522	Delta TCR V-J Junc	C	187	14.4	15.5	39	18	AAH89082	Primer for amplif
C	115	14.8	15.9	50	22	AAI30522	Human SNP oligonuc	C	188	14.4	15.5	40	19	AAH89082	Primer for amplif
C	116	14.8	15.9	50	22	AAI30522	Human SNP oligonuc	C	189	14.4	15.5	40	19	AAH89082	Primer for amplif
C	117	14.8	15.9	21	22	AAH76731	Human silent SNP c	C	190	14.4	15.5	41	16	AAH89082	Primer for amplif
C	118	14.6	15.7	21	22	AAH76731	PCR primer for hum	C	191	14.4	15.5	41	16	AAH89082	Primer for amplif
C	119	14.6	15.7	25	21	AAH8652	SNP specific lower	C	192	14.4	15.5	46	21	AAH89082	Primer for amplif
C	120	14.6	15.7	31	17	AAH8652	PCR primer DR3296	C	193	14.4	15.5	46	21	AAH89082	Primer for amplif
C	121	14.6	15.7	32	24	AAH8652	Primer for GAP pro	C	194	14.4	15.5	47	15	AAH89082	Primer for amplif
C	122	14.6	15.7	33	16	AAH8652	Human factor V DNA	C	195	14.4	15.5	47	15	AAH89082	Primer for amplif
C	123	14.6	15.7	33	16	AAH8652	Primer OL2 to crea	C	196	14.4	15.5	47	15	AAH89082	Primer for amplif
C	124	14.6	15.7	35	19	AAH8652	C-Jun amino acids	C	197	14.4	15.5	47	15	AAH89082	Primer for amplif
C	125	14.6	15.7	38	19	AAH8652	Fos amino acids 13	C	198	14.4	15.5	48	18	AAH89082	Primer for amplif
C	126	14.6	15.7	38	20	AAH8652	C. utilis crle PCR	C	199	14.4	15.5	48	18	AAH89082	Primer for amplif
C	127	14.6	15.7	39	20	AAH8652	PCR primer for GST	C	200	14.4	15.5	48	18	AAH89082	Primer for amplif
C	128	14.6	15.7	39	20	AAH8652	Thioredoxin specif	C	201	14.4	15.5	49	19	AAH89082	Primer for amplif
C	129	14.6	15.7	40	18	AAH8652	Sequence of CDNA p	C	202	14.4	15.5	49	19	AAH89082	Primer for amplif
C	130	14.6	15.7	40	18	AAH8652	Oligonucleotide Na	C	203	14.4	15.5	50	22	AAH89082	Primer for amplif
C	131	14.6	15.7	40	18	AAH8652	HBVcore-phosphota	C	204	14.4	15.5	50	22	AAH89082	Primer for amplif
C	132	14.6	15.7	40	22	AAH8652	PCR primer for DNA	C	205	14.4	15.5	50	22	AAH89082	Primer for amplif
C	133	14.6	15.7	40	22	AAH8652	Maize polymorphic	C	206	14.4	15.5	50	22	AAH89082	Primer for amplif
C	134	14.6	15.7	41	19	AAH8652	Human tyrosinase 1	C	207	14.4	15.5	50	22	AAH89082	Primer for amplif
C	135	14.6	15.7	41	24	AAH8652	Antibody kappa cha	C	208	14.4	15.5	50	22	AAH89082	Primer for amplif
C	136	14.6	15.7	43	20	AAH8652	Spinocerebellar at	C	209	14.4	15.5	50	22	AAH89082	Primer for amplif
C	137	14.6	15.7	44	16	AAH8652	Endonuclease stran	C	210	14.4	15.5	50	22	AAH89082	Primer for amplif
C	138	14.6	15.7	45	16	AAH8652	Human P703P peptid	C	211	14.4	15.5	50	22	AAH89082	Primer for amplif
C	139	14.6	15.7	45	22	AAH8652	Human GMCSF prim	C	212	14.4	15.5	50	22	AAH89082	Primer for amplif
C	140	14.6	15.7	45	22	AAH8652	Human GMCSF PCR pr	C	213	14.4	15.5	50	22	AAH89082	Primer for amplif
C	141	14.6	15.7	45	22	AAH8652	Human map-related	C	214	14.4	15.5	50	22	AAH89082	Primer for amplif
C	142	14.6	15.7	45	22	AAH8652	Rubella virus cDNA	C	215	14.4	15.5	50	22	AAH89082	Primer for amplif
C	143	14.6	15.7	47	15	AAH8652	Non-infectious tub	C	216	14.4	15.5	50	22	AAH89082	Primer for amplif
C	144	14.6	15.7	47	15	AAH8652	Plasmid pVLCNOVGH	C	217	14.4	15.5	50	22	AAH89082	Primer for amplif
C	145	14.6	15.7	47	15	AAH8652	Primer for fructos	C	218	14.4	15.5	50	22	AAH89082	Primer for amplif
C	146	14.6	15.7	48	19	AAH8652	Human DNAB4210 842	C	219	14.4	15.5	50	22	AAH89082	Primer for amplif
C	147	14.6	15.7	48	19	AAH8652	Influenza virus ge	C	220	14.4	15.5	50	22	AAH89082	Primer for amplif
C	148	14.6	15.7	48	19	AAH8652	PCR primer used fo	C	221	14.4	15.5	50	22	AAH89082	Primer for amplif
C	149	14.6	15.7	49	21	AAH8652	Human ACAM cDNA PC	C	222	14.4	15.5	50	22	AAH89082	Primer for amplif
C	150	14.6	15.7	50	14	AAH8652	NF-1 gene exon 5	C	223	14.4	15.5	50	22	AAH89082	Primer for amplif
C	151	14.6	15.7	50	14	AAH8652	Human SNP oligonuc	C	224	14.4	15.5	50	22	AAH89082	Primer for amplif
C	152	14.6	15.7	50	14	AAH8652	Human SNP oligonuc	C	225	14.4	15.5	50	22	AAH89082	Primer for amplif
C	153	14.6	15.7	50	14	AAH8652	Human SNP oligonuc	C	226	14.4	15.5	50	22	AAH89082	Primer for amplif
C	154	14.6	15.7	50	14	AAH8652	Human SNP oligonuc	C	227	14.4	15.5	50	22	AAH89082	Primer for amplif
C	155	14.6	15.7	50	14	AAH8652	Human SNP oligonuc	C	228	14.4	15.5	50	22	AAH89082	Primer for amplif

C 229	14.2	15.3	38	22	AAE77247	302	14	15.1	45	21	AAA74559	Alpha-conotoxin pr
C 230	14.2	15.3	39	21	AAE98828	303	14	15.1	45	21	AAA75757	Primer for DNA enc
C 231	14.2	15.3	40	15	AAO65789	304	14	15.1	45	21	AAA75758	Primer for DNA enc
C 232	14.2	15.3	40	19	AAV21699	305	14	15.1	45	22	AAV22580	Human PEO polypept
C 233	14.2	15.3	40	24	AB199100	306	14	15.1	45	24	AAV31478	Conus striatus S11
C 234	14.2	15.3	40	24	AB199264	307	14	15.1	47	21	AAV66348	Human map-related
C 235	14.2	15.3	41	24	AA142303	308	14	15.1	47	21	AAV67282	Human map-related
C 236	14.2	15.3	41	24	AA142304	309	14	15.1	47	21	AAV68817	Human map-related
C 237	14.2	15.3	42	21	AAV71124	310	14	15.1	47	21	AAV68817	Human map-related
C 238	14.2	15.3	42	21	AAV71132	311	14	15.1	47	21	AAV68817	Human map-related
C 239	14.2	15.3	45	20	AAV04173	312	14	15.1	47	23	AAV68817	Human map-related
C 240	14.2	15.3	47	21	AAV66398	313	14	15.1	48	24	AAV63250	CNS disorder-relat
C 241	14.2	15.3	47	21	AAV66396	314	14	15.1	48	24	AAV63250	Sequence of oligo
C 242	14.2	15.3	50	18	AAV67637	315	14	15.1	48	24	AAV63250	Human ERG ambrzym
C 243	14.2	15.3	50	22	AA130444	316	14	15.1	49	19	AAV63250	Plasmid pCMV/SB-N2
C 244	14.2	15.3	50	22	AA131207	317	14	15.1	49	21	AAV63250	Clone #7 fragment
C 245	14.2	15.3	50	22	AA132010	318	14	15.1	49	21	AAV63250	PCR primer v6 to o
C 246	14.2	15.3	50	22	AA178703	319	14	15.1	50	14	AAV63250	B. halodurans YesW
C 247	14.2	15.3	50	22	AAH90946	320	14	15.1	50	16	AAV63250	NF-1 gene exon 4 5
C 248	14.2	15.3	50	23	AB101075	321	14	15.1	50	19	AAV63250	P-selectin ligand/
C 249	14.2	15.3	50	23	AB101075	322	14	15.1	50	19	AAV63250	Human P-selectin 1
C 250	14.2	15.3	50	24	ABN72455	323	14	15.1	50	20	AAV63250	Downstream primer
C 251	14.2	15.1	23	21	AAV59258	324	14	15.1	50	20	AAV63250	P-selectin ligand
C 252	14.2	15.1	23	22	AAV59258	325	14	15.1	50	20	AAV63250	Synthetic plasmid
C 253	14.2	15.1	24	24	ABO00510	326	14	15.1	50	20	AAV63250	Human P-selectin 1
C 254	14.2	15.1	24	24	ABO01251	327	14	15.1	50	22	AA130003	Human SGP oligonuc
C 255	14.2	15.1	24	24	ABO04984	328	14	15.1	50	22	AA130003	Human SGP oligonuc
C 256	14.2	15.1	24	24	ABO06452	329	14	15.1	50	22	AA130003	Human SGP oligonuc
C 257	14.2	15.1	24	24	ABO06452	330	14	15.1	50	22	AA130003	Human SGP oligonuc
C 258	14.2	15.1	24	24	ABO06452	331	14	15.1	50	22	AA130003	Human SGP oligonuc
C 259	14.2	15.1	24	24	ABO06452	332	14	15.1	50	22	AA130003	Human SGP oligonuc
C 260	14.2	15.1	24	24	ABO06452	333	14	15.1	50	22	AA130003	Human SGP oligonuc
C 261	14.2	15.1	24	24	ABO06452	334	14	15.1	50	22	AA130003	Human SGP oligonuc
C 262	14.2	15.1	24	24	ABO06452	335	14	15.1	50	22	AA130003	Human SGP oligonuc
C 263	14.2	15.1	24	24	ABO06452	336	14	15.1	50	22	AA130003	Human SGP oligonuc
C 264	14.2	15.1	24	24	ABO06452	337	14	15.1	50	22	AA130003	Human SGP oligonuc
C 265	14.2	15.1	24	24	ABO06452	338	14	15.1	50	22	AA130003	Human SGP oligonuc
C 266	14.2	15.1	24	24	ABO06452	339	14	15.1	50	22	AA130003	Human SGP oligonuc
C 267	14.2	15.1	24	24	ABO06452	340	14	15.1	50	22	AA130003	Human SGP oligonuc
C 268	14.2	15.1	24	24	ABO06452	341	14	15.1	50	22	AA130003	Human SGP oligonuc
C 269	14.2	15.1	24	24	ABO06452	342	14	15.1	50	22	AA130003	Human SGP oligonuc
C 270	14.2	15.1	24	24	ABO06452	343	14	15.1	50	22	AA130003	Human SGP oligonuc
C 271	14.2	15.1	24	24	ABO06452	344	14	15.1	50	22	AA130003	Human SGP oligonuc
C 272	14.2	15.1	24	24	ABO06452	345	14	15.1	50	22	AA130003	Human SGP oligonuc
C 273	14.2	15.1	24	24	ABO06452	346	14	15.1	50	22	AA130003	Human SGP oligonuc
C 274	14.2	15.1	24	24	ABO06452	347	14	15.1	50	22	AA130003	Human SGP oligonuc
C 275	14.2	15.1	24	24	ABO06452	348	14	15.1	50	22	AA130003	Human SGP oligonuc
C 276	14.2	15.1	24	24	ABO06452	349	14	15.1	50	22	AA130003	Human SGP oligonuc
C 277	14.2	15.1	24	24	ABO06452	350	14	15.1	50	22	AA130003	Human SGP oligonuc
C 278	14.2	15.1	24	24	ABO06452	351	14	15.1	50	22	AA130003	Human SGP oligonuc
C 279	14.2	15.1	24	24	ABO06452	352	14	15.1	50	22	AA130003	Human SGP oligonuc
C 280	14.2	15.1	24	24	ABO06452	353	14	15.1	50	22	AA130003	Human SGP oligonuc
C 281	14.2	15.1	24	24	ABO06452	354	14	15.1	50	22	AA130003	Human SGP oligonuc
C 282	14.2	15.1	24	24	ABO06452	355	14	15.1	50	22	AA130003	Human SGP oligonuc
C 283	14.2	15.1	24	24	ABO06452	356	14	15.1	50	22	AA130003	Human SGP oligonuc
C 284	14.2	15.1	24	24	ABO06452	357	14	15.1	50	22	AA130003	Human SGP oligonuc
C 285	14.2	15.1	24	24	ABO06452	358	14	15.1	50	22	AA130003	Human SGP oligonuc
C 286	14.2	15.1	24	24	ABO06452	359	14	15.1	50	22	AA130003	Human SGP oligonuc
C 287	14.2	15.1	24	24	ABO06452	360	14	15.1	50	22	AA130003	Human SGP oligonuc
C 288	14.2	15.1	24	24	ABO06452	361	14	15.1	50	22	AA130003	Human SGP oligonuc
C 289	14.2	15.1	24	24	ABO06452	362	14	15.1	50	22	AA130003	Human SGP oligonuc
C 290	14.2	15.1	24	24	ABO06452	363	14	15.1	50	22	AA130003	Human SGP oligonuc
C 291	14.2	15.1	24	24	ABO06452	364	14	15.1	50	22	AA130003	Human SGP oligonuc
C 292	14.2	15.1	24	24	ABO06452	365	14	15.1	50	22	AA130003	Human SGP oligonuc
C 293	14.2	15.1	24	24	ABO06452	366	14	15.1	50	22	AA130003	Human SGP oligonuc
C 294	14.2	15.1	24	24	ABO06452	367	14	15.1	50	22	AA130003	Human SGP oligonuc
C 295	14.2	15.1	24	24	ABO06452	368	14	15.1	50	22	AA130003	Human SGP oligonuc
C 296	14.2	15.1	24	24	ABO06452	369	14	15.1	50	22	AA130003	Human SGP oligonuc
C 297	14.2	15.1	24	24	ABO06452	370	14	15.1	50	22	AA130003	Human SGP oligonuc
C 298	14.2	15.1	24	24	ABO06452	371	14	15.1	50	22	AA130003	Human SGP oligonuc
C 299	14.2	15.1	24	24	ABO06452	372	14	15.1	50	22	AA130003	Human SGP oligonuc
C 300	14.2	15.1	24	24	ABO06452	373	14	15.1	50	22	AA130003	Human SGP oligonuc
C 301	14.2	15.1	24	24	ABO06452	374	14	15.1	50	22	AA130003	Human SGP oligonuc

C 375	13.8	14.8	45	16	AAT26019	Human gene signatu	C 448	13.6	14.6	41	24	AAK98855	Protein 2 of the hum
C 376	13.8	14.8	45	22	AAD02419	Pichia methanolica	C 449	13.6	14.6	41	24	ABA97056	Human 2-hydroxy ac
C 377	13.8	14.8	46	15	AAO69385	Human fibrinogen b	C 450	13.6	14.6	41	24	ABA97057	Human 2-hydroxy ac
C 378	13.8	14.8	46	15	AAO71361	Antisense PCR prim	C 451	13.6	14.6	42	15	AAO69426	Human gene for cla
C 379	13.8	14.8	46	18	AAT63847	Human fibrinogen b	C 452	13.6	14.6	42	15	AAO69426	Human HLA-CW3 gene
C 380	13.8	14.8	46	20	AAI17135	Test sequence from	C 453	13.6	14.6	42	20	AAI17176	Test sequence from
C 381	13.8	14.8	46	22	AAH39052	Human SNP flanking	C 454	13.6	14.6	42	20	AAI17176	Murine TNF-alpha g
C 382	13.8	14.8	46	24	AAK82626	DNA binding molecu	C 455	13.6	14.6	42	24	AAI47180	Murine TNF-alpha g
C 383	13.8	14.8	47	14	AAO34899	PCR primer #56 use	C 456	13.6	14.6	42	24	AAK82627	DNA binding molecu
C 384	13.8	14.8	47	14	AAO34905	PCR primer #62 use	C 457	13.6	14.6	43	18	AAT73221	HSV-1 glycoprotein
C 385	13.8	14.8	47	14	AAO34911	PCR primer #68 use	C 458	13.6	14.6	45	16	AAO94175	Transmembrane olig
C 386	13.8	14.8	47	14	AAO34917	PCR primer #74 use	C 459	13.6	14.6	45	24	AAI47502	HPV type 18 L1-E7
C 387	13.8	14.8	47	21	AAZ66272	Human map-related	C 460	13.6	14.6	45	24	AAI47502	HPV type 18 L1-E7
C 388	13.8	14.8	47	21	AAZ66272	Yeast HA-gal12 rev	C 461	13.6	14.6	45	24	AAI47502	HPV type 18 L1-E7
C 389	13.8	14.8	48	18	AAT97348	Mouse CCRP recepto	C 462	13.6	14.6	46	20	AAV72467	Human PRO33 clone
C 390	13.8	14.8	48	24	AAI68914	Activated T-cell d	C 463	13.6	14.6	46	20	AAI68914	Human PRO33 clone
C 391	13.8	14.8	49	21	AAO08724	Human secreted pro	C 464	13.6	14.6	46	20	AAI68914	Human PRO33 clone
C 392	13.8	14.8	49	24	AAK15676	PRA2 vector casset	C 465	13.6	14.6	46	21	AAI68914	Human PRO33 clone
C 393	13.8	14.8	50	9	AAO06029	Probe (b) for the	C 466	13.6	14.6	46	21	AAI68914	Human PRO33 clone
C 394	13.8	14.8	50	19	AAV11484	T. halophilus xylo	C 467	13.6	14.6	46	22	AAI68914	Human PRO33 clone
C 395	13.8	14.8	50	20	AAV91198	M. smegmatis 16S r	C 468	13.6	14.6	46	22	AAI68914	Human PRO33 clone
C 396	13.8	14.8	50	22	AAI29876	Human SNP oligonuc	C 469	13.6	14.6	47	21	AAI68914	Human PRO33 clone
C 397	13.8	14.8	50	22	AAI29877	Human SNP oligonuc	C 470	13.6	14.6	47	21	AAI68914	Human PRO33 clone
C 398	13.8	14.8	50	22	AAI30605	Human SNP oligonuc	C 471	13.6	14.6	47	21	AAI68914	Human PRO33 clone
C 399	13.8	14.8	50	22	AAI34461	Human SNP oligonuc	C 472	13.6	14.6	47	21	AAI68914	Human PRO33 clone
C 400	13.8	14.8	50	22	AAI28354	Nucleotide sequenc	C 473	13.6	14.6	47	23	AAH88586	Human map-related
C 401	13.6	14.6	20	20	AAO1894	PCR primer used to	C 474	13.6	14.6	48	22	AAH88586	Human map-related
C 402	13.6	14.6	20	21	AAI41227	Human TTRalpha ant	C 475	13.6	14.6	48	22	AAH88586	Human map-related
C 403	13.6	14.6	20	22	AAO89583	S. cerevisiae YFR0	C 476	13.6	14.6	48	22	AAH88586	Human map-related
C 404	13.6	14.6	20	22	AAO89583	S. cerevisiae YFR0	C 477	13.6	14.6	48	22	AAH88586	Human map-related
C 405	13.6	14.6	20	22	AAO89583	S. cerevisiae YFR0	C 478	13.6	14.6	48	22	AAH88586	Human map-related
C 406	13.6	14.6	20	22	AAO89583	S. cerevisiae YFR0	C 479	13.6	14.6	48	22	AAH88586	Human map-related
C 407	13.6	14.6	21	19	AAV55954	Human caspase 2 an	C 480	13.6	14.6	48	22	AAH88586	Human map-related
C 408	13.6	14.6	21	19	AAV55954	Chimeric C/EBP jun	C 481	13.6	14.6	48	22	AAH88586	Human map-related
C 409	13.6	14.6	21	19	AAV55954	PCR primer derived	C 482	13.6	14.6	48	22	AAH88586	Human map-related
C 410	13.6	14.6	21	19	AAV55954	Oligonucleotide #1	C 483	13.6	14.6	48	22	AAH88586	Human map-related
C 411	13.6	14.6	21	19	AAV55954	Lac protease relat	C 484	13.6	14.6	48	22	AAH88586	Human map-related
C 412	13.6	14.6	21	19	AAV55954	Yeast HMG-CoA redu	C 485	13.6	14.6	48	22	AAH88586	Human map-related
C 413	13.6	14.6	21	19	AAV55954	Homo sapiens DNA c	C 486	13.6	14.6	48	22	AAH88586	Human map-related
C 414	13.6	14.6	21	19	AAV55954	Reverse primer TLI	C 487	13.6	14.6	48	22	AAH88586	Human map-related
C 415	13.6	14.6	21	19	AAV55954	Br-2 plasmid PCR p	C 488	13.6	14.6	48	22	AAH88586	Human map-related
C 416	13.6	14.6	21	19	AAV55954	Human secreted pro	C 489	13.6	14.6	48	22	AAH88586	Human map-related
C 417	13.6	14.6	21	19	AAV55954	Human TIE-2 hammer	C 490	13.6	14.6	48	22	AAH88586	Human map-related
C 418	13.6	14.6	21	19	AAV55954	Human TIE-2 hammer	C 491	13.6	14.6	48	22	AAH88586	Human map-related
C 419	13.6	14.6	21	19	AAV55954	Hammerhead ribozym	C 492	13.6	14.6	48	22	AAH88586	Human map-related
C 420	13.6	14.6	21	19	AAV55954	Hammerhead ribozym	C 493	13.6	14.6	48	22	AAH88586	Human map-related
C 421	13.6	14.6	21	19	AAV55954	Hammerhead ribozym	C 494	13.6	14.6	48	22	AAH88586	Human map-related
C 422	13.6	14.6	21	19	AAV55954	Oestrogen receptor	C 495	13.6	14.6	48	22	AAH88586	Human map-related
C 423	13.6	14.6	21	19	AAV55954	Human inflammatory	C 496	13.6	14.6	48	22	AAH88586	Human map-related
C 424	13.6	14.6	21	19	AAV55954	Human inflammatory	C 497	13.6	14.6	48	22	AAH88586	Human map-related
C 425	13.6	14.6	21	19	AAV55954	Sense primer to am	C 498	13.6	14.6	48	22	AAH88586	Human map-related
C 426	13.6	14.6	21	19	AAV55954	HTRT sequence-spec	C 499	13.6	14.6	48	22	AAH88586	Human map-related
C 427	13.6	14.6	21	19	AAV55954	Human genomic DNA	C 500	13.6	14.6	48	22	AAH88586	Human map-related
C 428	13.6	14.6	21	19	AAV55954	A. orientalis NRRL	C 501	13.6	14.6	48	22	AAH88586	Human map-related
C 429	13.6	14.6	21	19	AAV55954	Human allergic dis	C 502	13.6	14.6	48	22	AAH88586	Human map-related
C 430	13.6	14.6	21	19	AAV55954	Human tumour vascu	C 503	13.6	14.6	48	22	AAH88586	Human map-related
C 431	13.6	14.6	21	19	AAV55954	Reproductive recom	C 504	13.6	14.6	48	22	AAH88586	Human map-related
C 432	13.6	14.6	21	19	AAV55954	Myelin P0 protein	C 505	13.6	14.6	48	22	AAH88586	Human map-related
C 433	13.6	14.6	21	19	AAV55954	Alpha-5 subunit pr	C 506	13.6	14.6	48	22	AAH88586	Human map-related
C 434	13.6	14.6	21	19	AAV55954	Human GABA recepto	C 507	13.6	14.6	48	22	AAH88586	Human map-related
C 435	13.6	14.6	21	19	AAV55954	Probe 1105 for the	C 508	13.6	14.6	48	22	AAH88586	Human map-related
C 436	13.6	14.6	21	19	AAV55954	PCR primer OPM1 to	C 509	13.6	14.6	48	22	AAH88586	Human map-related
C 437	13.6	14.6	21	19	AAV55954	PCR primer used to	C 510	13.6	14.6	48	22	AAH88586	Human map-related
C 438	13.6	14.6	21	19	AAV55954	E. coli phosphopan	C 511	13.6	14.6	48	22	AAH88586	Human map-related
C 439	13.6	14.6	21	19	AAV55954	Human Chk1 ribozym	C 512	13.6	14.6	48	22	AAH88586	Human map-related
C 440	13.6	14.6	21	19	AAV55954	Human BRC1 intera	C 513	13.6	14.6	48	22	AAH88586	Human map-related
C 441	13.6	14.6	21	19	AAV55954	Human epidermal gr	C 514	13.6	14.6	48	22	AAH88586	Human map-related
C 442	13.6	14.6	21	19	AAV55954	Fragment of cDNA e	C 515	13.6	14.6	48	22	AAH88586	Human map-related
C 443	13.6	14.6	21	19	AAV55954	Human keratinocyte	C 516	13.6	14.6	48	22	AAH88586	Human map-related
C 444	13.6	14.6	21	19	AAV55954	Maize polymorphic	C 517	13.6	14.6	48	22	AAH88586	Human map-related
C 445	13.6	14.6	21	19	AAV55954	Human p53DGC hypr	C 518	13.6	14.6	48	22	AAH88586	Human map-related
C 446	13.6	14.6	21	19	AAV55954	hNKG DNA cloning p	C 519	13.6	14.6	48	22	AAH88586	Human map-related
C 447	13.6	14.6	21	19	AAV55954	Human Na-dependent	C 520	13.6	14.6	48	22	AAH88586	Human map-related
C 448	13.6	14.6	21	19	AAV55954	Serine proteinase	C 521	13.6	14.6	48	22	AAH88586	Human map-related
C 449	13.6	14.6	21	19	AAV55954	Serine proteinase	C 522	13.6	14.6	48	22	AAH88586	Human map-related
C 450	13.6	14.6	21	19	AAV55954	Serine proteinase	C 523	13.6	14.6	48	22	AAH88586	Human map-related
C 451	13.6	14.6	21	19	AAV55954	Serine proteinase	C 524	13.6	14.6	48	22	AAH88586	Human map-related
C 452	13.6	14.6	21	19	AAV55954	Serine proteinase	C 525	13.6	14.6	48	22	AAH88586	Human map-related
C 453	13.6	14.6	21	19	AAV55954	Serine proteinase	C 526	13.6	14.6	48	22	AAH88586	Human map-related
C 454	13.6	14.6	21	19	AAV55954	Serine proteinase	C 527	13.6	14.6	48	22	AAH88586	Human map-related
C 455	13.6	14.6	21	19	AAV55954	Serine proteinase	C 528	13.6	14.6	48	22	AAH88586	Human map-related
C 456	13.6	14.6	21	19	AAV55954	Serine proteinase	C 529	13.6	14.6	48	22	AAH88586	Human map-related
C 457	13.6	14.6	21	19	AAV55954	Serine proteinase	C 530	13.6	14.6	48	22	AAH88586	Human map-related
C 458	13.6	14.6	21	19	AAV55954	Serine proteinase	C 531	13.6	14.6	48	22	AAH88586	Human map-related
C 459	13.6	14.6	21	19	AAV55954	Serine proteinase	C 532	13.6	14.6	48	22	AAH88586	Human map-related
C 460	13.6	14.6	21	19	AAV55954	Serine proteinase	C 533	13.6	14.6	48	22	AAH88586	Human map-related
C 461	13.6	14.6	21	19	AAV55954	Serine proteinase	C 534	13.6	14.6	48	22	AAH88586	Human map-related
C 462	13.6	14.6	21	19	AAV55954	Serine proteinase	C 535	13.6	14.6	48	22	AAH88586	Human map-related
C 463	13.6	14.6	21	19	AAV55954	Serine proteinase	C 536	13.6	14.6	48	22	AAH88586	Human map-related
C 464	13.6	14.6	21	19	AAV55954	Serine proteinase	C 537	13.6	14.6	48	22	AAH88586	Human map-related
C 465	13.6	14.6	21	19	AAV55954	Serine proteinase	C 538	13.6	14.6	48	22	AAH88586	Human map-related
C 466	13.6	14.6	21	19	AAV55954	Serine proteinase	C 539	13.6	14.6	48	22	AAH88586	Human map-related
C 467	13.6	14.6	21	19	AAV55954	Serine proteinase	C 540	13.6	14.6	48	22	AAH88586	Human map-related
C 468	13.6	14.6	21	19	AAV55954	Serine proteinase							

C 521	13.4	14.4	33	24	ABN85532	Human calmodulin 9	C 594	13.4	14.4	48	20	AAK25648	IL-2/FasL fusion h
C 522	13.4	14.4	33	24	ABN94064	Human neuropeptide	C 595	13.4	14.4	48	23	ABK07410	Human NOGO Amberry
C 523	13.4	14.4	33	24	ABN18181	Human proliferatin	C 596	13.4	14.4	48	23	ABK07596	Human NOGO Amberry
C 524	13.4	14.4	33	24	ABN95826	IL retrotranscript	C 597	13.4	14.4	48	23	ABK09204	Human CD20 Amberry
C 525	13.4	14.4	33	24	ABN05039	Human ATP-dependent	C 598	13.4	14.4	48	24	ABD28877	Human antibody J 1
C 526	13.4	14.4	34	18	AAAT91689	Acetomolium cellulo	C 599	13.4	14.4	49	12	AAO12206	Sequence encoding
C 527	13.4	14.4	35	18	AAO11430	Probe 1530 specifi	C 600	13.4	14.4	49	16	AAO28888	Novel target nucle
C 528	13.4	14.4	35	18	AAAT45022	Primer used in con	C 601	13.4	14.4	50	20	AAK52195	Synthetic plasmid
C 529	13.4	14.4	35	19	AAV36390	PCR primer 5 ampli	C 602	13.4	14.4	50	20	AAK52183	Synthetic plasmid
C 530	13.4	14.4	35	19	AAV36391	PCR primer 6 ampli	C 603	13.4	14.4	50	20	AAK52050	Synthetic plasmid
C 531	13.4	14.4	36	20	AAK03351	Reverse PCR primer	C 604	13.4	14.4	50	22	AAK28607	Human SNP oligonuc
C 532	13.4	14.4	36	20	AAK55205	Neisseria species	C 605	13.4	14.4	50	22	AAK30621	Human SNP oligonuc
C 533	13.4	14.4	38	17	AAAT40779	Primer for CRPV L1	C 606	13.4	14.4	50	22	AAK30622	Human SNP oligonuc
C 534	13.4	14.4	38	18	AAAT65043	5'-primer #1 for x	C 607	13.4	14.4	50	22	AAK37716	Human SNP oligonuc
C 535	13.4	14.4	38	18	AAAT61434	Oligonucleotide L-	C 608	13.4	14.4	50	22	AAK34283	Human SNP oligonuc
C 536	13.4	14.4	38	21	AAAG4102	Nucleotide sequenc	C 609	13.4	14.4	50	22	AAK177513	Human silent SNP c
C 537	13.4	14.4	38	21	AAZ43902	M. tuberculosis rp	C 610	13.4	14.4	50	22	AAH77532	Probe oligonucleot
C 538	13.4	14.4	39	19	AAV29975	PCR primer used to	C 611	13.4	14.4	50	22	AAH90294	Human clone cg4412
C 539	13.4	14.4	39	21	AAH87253	Rat hepatocyte car	C 612	13.4	14.4	50	22	AAH90296	Human clone cg4412
C 540	13.4	14.4	39	22	AAK43779	T cell receptor TC	C 613	13.4	14.4	50	22	AAH00218	Human silent nonco
C 541	13.4	14.4	39	22	AAK30071	Human epidermal gr	C 614	13.4	14.4	50	23	AAO71129	Merlin exon 7 prim
C 542	13.4	14.4	40	16	AAO89095	Elastase DNA nucle	C 615	13.2	14.2	20	15	AAO71129	Primer #1 for Hyg
C 543	13.4	14.4	40	16	AAO89113	Elastase DNA nucle	C 616	13.2	14.2	20	16	AAZ01609	PCR primer used to
C 544	13.4	14.4	40	20	AAK91481	T. gondii immunoge	C 617	13.2	14.2	20	20	AAK96067	PCR primer used to
C 545	13.4	14.4	40	22	AAK42804	Dengue-3 virus der	C 618	13.2	14.2	20	20	AAK93226	PCR primer used to
C 546	13.4	14.4	40	22	AAK83817	Human mannosidase	C 619	13.2	14.2	20	21	AAK81429	Human T-krappa-B k
C 547	13.4	14.4	40	22	AAK14778	Human mannosidase	C 620	13.2	14.2	20	21	AAK41113	Human T-krappa-B k
C 548	13.4	14.4	41	18	AAK95359	Mouse anti-PlpA MA	C 621	13.2	14.2	20	21	AAK11944	Human MDMK antisen
C 549	13.4	14.4	41	22	AAI69568	Bromo-structure do	C 622	13.2	14.2	20	22	AAH77796	PCR primer for mur
C 550	13.4	14.4	41	22	AAO20168	P. futilculosum csi	C 623	13.2	14.2	21	20	AAH86419	PCR primer PDZK.6
C 551	13.4	14.4	41	24	ABK88048	Dihydrofolate redu	C 624	13.2	14.2	21	21	AAH62171	Phosphorylates glyc
C 552	13.4	14.4	41	24	ABK55361	Human protein synt	C 625	13.2	14.2	21	22	AAK55176	Probe used to iden
C 553	13.4	14.4	41	24	ABK10785	Human genetic mult	C 626	13.2	14.2	22	24	AAO50001	PCR primer p2 to a
C 554	13.4	14.4	41	24	ABK10785	Human genetic mult	C 627	13.2	14.2	22	24	AAO29279	Human CRM-2 ampli
C 555	13.4	14.4	41	24	ABK10785	Human genetic mult	C 628	13.2	14.2	22	24	AAK91352	Primer for RT-PCR
C 556	13.4	14.4	41	24	ABK98007	Human p2cd6 prote	C 629	13.2	14.2	23	20	AAK42675	T. gondii immunoge
C 557	13.4	14.4	41	24	ABK98008	Human p2cd6 prote	C 630	13.2	14.2	23	22	AAK42675	Human hypoxanthine
C 558	13.4	14.4	41	24	AAI18833	Non-natural base P	C 631	13.2	14.2	24	18	AAK79008	Human HPT exon 3
C 559	13.4	14.4	41	24	AAI66351	Human alpha-galact	C 632	13.2	14.2	24	19	AAK69298	Mouse adipose tiss
C 560	13.4	14.4	42	16	AAO80759	Pilot oligonucleot	C 633	13.2	14.2	24	20	AAZ38119	Corrected neo gene
C 561	13.4	14.4	42	16	AAO808198	Amplification prim	C 634	13.2	14.2	24	21	AAK43289	HIV-1 type M speci
C 562	13.4	14.4	42	18	AAAT70338	Pilot oligonucleot	C 635	13.2	14.2	24	24	AAH44913	PCR primer #1 for
C 563	13.4	14.4	42	18	AAAT76638	Pilot oligonucleot	C 636	13.2	14.2	25	24	AAK56603	Strawberry alcohol
C 564	13.4	14.4	42	19	AAV53862	Oligonucleotide 30	C 637	13.2	14.2	25	21	AAK96863	HIA HIA-C gene PCR
C 565	13.4	14.4	42	19	AAV53862	Nucleotide sequenc	C 638	13.2	14.2	25	21	AAK27679	Strawberry alcohol
C 566	13.4	14.4	42	20	AAK07213	Retroviral 3' U3-R	C 639	13.2	14.2	25	21	AAK11960	Human momp-2 assoc
C 567	13.4	14.4	43	21	AAV63414	Pilot oligonucleot	C 640	13.2	14.2	26	22	AAH44901	HIV specific prime
C 568	13.4	14.4	43	21	AAV63414	Single base extens	C 641	13.2	14.2	26	22	AAK32217	Human Musashi 1 PC
C 569	13.4	14.4	44	18	AAI9180	Human major histoc	C 642	13.2	14.2	26	24	ABK66425	Human gene specifi
C 570	13.4	14.4	44	24	ABN97214	Immunoglobulin lam	C 643	13.2	14.2	27	24	ABK67164	Human gene specifi
C 571	13.4	14.4	45	21	AAK63367	E2F binding/inhibi	C 644	13.2	14.2	28	17	AAK28472	S. saprophyticus d
C 572	13.4	14.4	45	19	AAV10117	Human H11-scrv kap	C 645	13.2	14.2	28	22	AAK75923	Staphylococcus sap
C 573	13.4	14.4	46	20	AAK31577	PCR primer for pec	C 646	13.2	14.2	28	24	ABK48690	Mouse intron 9 5'
C 574	13.4	14.4	46	20	AAK03871	FCV capsid/beta-ga	C 647	13.2	14.2	29	20	AAK19860	Integrin alpha 6 s
C 575	13.4	14.4	46	22	AAK04536	Human H11-scrv sin	C 648	13.2	14.2	29	20	AAV93040	Human B-rat hamme
C 576	13.4	14.4	47	19	AAV56434	Human ICAM-R CDNA	C 649	13.2	14.2	29	21	AAK55273	Neisseria species
C 577	13.4	14.4	47	19	AAV54870	PCR primer 88 used	C 650	13.2	14.2	30	16	AAK17802	Angiotensin II DNA
C 578	13.4	14.4	47	20	AAK21889	Primer for antibody	C 651	13.2	14.2	30	21	AAK31891	Lck SH2 cDNA fragm
C 579	13.4	14.4	47	20	AAV69202	Chimeric ICR-1.1 a	C 652	13.2	14.2	30	21	AAK22708	Human HSP70 gene p
C 580	13.4	14.4	47	21	AAK66478	Human map-related	C 653	13.2	14.2	30	22	AAK27589	Novel signal trans
C 581	13.4	14.4	47	21	AAK66534	Human map-related	C 654	13.2	14.2	30	22	AAK73599	HRF nucleic acid I
C 582	13.4	14.4	47	21	AAK67506	Human map-related	C 655	13.2	14.2	30	22	ABK88853	Green fluorescent
C 583	13.4	14.4	47	21	AAK67680	Human map-related	C 656	13.2	14.2	30	24	ABK91978	Mouse tensascin PCR
C 584	13.4	14.4	47	21	AAK68075	Human map-related	C 657	13.2	14.2	31	11	AAO03646	Probe IF-11 for CD
C 585	13.4	14.4	47	21	AAK69295	Human map-related	C 658	13.2	14.2	31	20	AAK06206	Human biallelic po
C 586	13.4	14.4	47	21	AAK91716	PCR primer 88 used	C 659	13.2	14.2	31	24	AAK35606	Tobacco rattle vir
C 587	13.4	14.4	47	21	AAK57692	PCR primer for det	C 660	13.2	14.2	31	24	ABK92083	Tobacco rattle vir
C 588	13.4	14.4	47	21	AAK08322	Chimeric ICR-1.1 a	C 661	13.2	14.2	31	24	ABK12033	p2-2 PCR primer fo
C 589	13.4	14.4	47	21	AAK24348	Chimerised murine	C 662	13.2	14.2	31	24	ABK93969	Influenza A/tdorn/
C 590	13.4	14.4	47	22	AAH46327	Anti-SPC antibody	C 663	13.2	14.2	32	9	AAK08081	Probe no. 2 for CnI
C 591	13.4	14.4	47	22	AAH88300	CNS disorder-relat	C 664	13.2	14.2	32	22	AAK29614	Pseudomonas aerugi
C 592	13.4	14.4	47	23	AAH88657	CNS disorder-relat	C 665	13.2	14.2	32	22	AAK29614	C. trachomatis rRN
C 593	13.4	14.4	48	13	AAO23822	Primer HuJlambd4-	C 666	13.2	14.2	33	13	AAO30195	Sequence of PCR pr

c 667	13.2	14.2	33	14	AA045990	Ribozyme cleavage	c 740	13.2	14.2	47	21	AA65698	Human map-related
c 668	13.2	14.2	33	19	AAV54343	T-cell receptor V-	c 741	13.2	14.2	47	21	AA67071	Human map-related
c 669	13.2	14.2	33	20	AAZ34517	Human LYSF-2 bait	c 742	13.2	14.2	47	21	AA67681	Human map-related
c 670	13.2	14.2	33	20	AAV55426	Primer to amplify	c 743	13.2	14.2	47	21	AA68334	Human map-related
c 671	13.2	14.2	33	21	AA61359	RNA substrate stra	c 744	13.2	14.2	47	21	AA68802	Human map-related
c 672	13.2	14.2	33	22	AAV77417	HIV-1 RNA sequence	c 745	13.2	14.2	47	21	AA69056	Human map-related
c 673	13.2	14.2	33	23	AB197678	Endogenous human G	c 746	13.2	14.2	47	22	AA69239	Sample member clus
c 674	13.2	14.2	33	24	AA138117	Angiogenesis gene	c 747	13.2	14.2	47	22	AA687453	Sendai virus M-F s
c 675	13.2	14.2	33	24	AA172751	Human excitatory a	c 748	13.2	14.2	47	22	AA687454	Sendai virus M-F s
c 676	13.2	14.2	33	24	ABK47407	Human mitochondria	c 749	13.2	14.2	47	22	AA687505	Sendai virus M-F s
c 677	13.2	14.2	33	24	AB142397	HistH1y1-tRNA synt	c 750	13.2	14.2	47	22	AA687506	Sendai virus M-F s
c 678	13.2	14.2	33	24	ABR01927	Human uterine glob	c 751	13.2	14.2	47	22	AA633990	Sense primer used
c 679	13.2	14.2	34	15	AA037263	Enzymatic RNA mole	c 752	13.2	14.2	47	24	AA633991	Antisense primer u
c 680	13.2	14.2	34	15	AAV35780	PCR primer IL8P1 o	c 753	13.2	14.2	47	24	AA621184	Neurofilament-L (N
c 681	13.2	14.2	35	17	AA14896	Primer 2 for porci	c 754	13.2	14.2	48	16	AA637453	Primer JK5FORNOR.
c 682	13.2	14.2	35	17	AA129978	Substrate RNA (S2)	c 755	13.2	14.2	48	16	AA094182	Transmembrane olig
c 683	13.2	14.2	35	18	AA147522	Transforming growt	c 756	13.2	14.2	48	20	AAV03964	LOR probe G6Dex6-
c 684	13.2	14.2	35	19	AAV35384	Human INOS DNA PCR	c 757	13.2	14.2	48	20	AAV76648	Human SPV library
c 685	13.2	14.2	35	20	AA332096	HIMOS 5'-flanking	c 758	13.2	14.2	48	21	AA113521	Xi exchange unit D
c 686	13.2	14.2	36	3	AAV20113	Junction between a	c 759	13.2	14.2	48	22	AA113488	Human LTV-1-164647
c 687	13.2	14.2	36	18	AA147524	Human hepatoma-der	c 760	13.2	14.2	48	22	AA130030	Human Interleukin
c 688	13.2	14.2	36	22	AA157507	E. coli TEM1 gene	c 761	13.2	14.2	48	24	AA130030	PCR primer HuJ5FO
c 689	13.2	14.2	36	22	AA157507	T reesei cellbioh	c 762	13.2	14.2	49	22	AA157507	Human antibody J k
c 690	13.2	14.2	36	22	AA157507	T reesei cellbioh	c 763	13.2	14.2	49	22	AA157507	Human oestrogen re
c 691	13.2	14.2	36	22	AA157507	Aspergillus niger	c 764	13.2	14.2	49	22	AA157507	Human oestrogen re
c 692	13.2	14.2	36	24	AB154686	Lactobacillus 235	c 765	13.2	14.2	49	24	AA157507	MAGE-1 DNA fragmen
c 693	13.2	14.2	37	19	AAV55606	LRP5 exon primer E	c 766	13.2	14.2	50	20	AA157507	Human PRO35 detec
c 694	13.2	14.2	38	14	AA048779	Apodrosin primer	c 767	13.2	14.2	50	20	AA157507	Probe used to iso
c 695	13.2	14.2	38	14	AA049216	Hamster Apodrosin	c 768	13.2	14.2	50	20	AA157507	Probe used to iso
c 696	13.2	14.2	38	19	AAV61827	PCR primer for hum	c 769	13.2	14.2	50	21	AA157507	Human clone c94400
c 697	13.2	14.2	38	19	AAV44489	CRNA-Lys3 pseudoge	c 770	13.2	14.2	50	21	AA157507	Human SNP oligonuc
c 698	13.2	14.2	38	19	AAV35561	Human Interleukin	c 771	13.2	14.2	50	22	AA128970	Human SNP oligonuc
c 699	13.2	14.2	38	22	AA681261	Primer BsyGK-62 fo	c 772	13.2	14.2	50	22	AA128970	Human SNP oligonuc
c 700	13.2	14.2	38	22	AA681261	Human Interleukin	c 773	13.2	14.2	50	22	AA128970	Human SNP oligonuc
c 701	13.2	14.2	38	23	ABK05651	Human NOGO zinzyme	c 774	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 702	13.2	14.2	39	19	AAV18089	Human liver ribonu	c 775	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 703	13.2	14.2	39	21	AAV73447	Single base extens	c 776	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 704	13.2	14.2	39	24	ABR91336	Streptococcus dysg	c 777	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 705	13.2	14.2	40	21	AAV73431	Single base extens	c 778	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 706	13.2	14.2	40	21	AAV73431	Primer specific fo	c 779	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 707	13.2	14.2	40	24	AB199213	Green/red click be	c 780	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 708	13.2	14.2	41	19	AAV51024	Maize polymorphic	c 781	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 709	13.2	14.2	41	19	AAV51025	Maize polymorphic	c 782	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 710	13.2	14.2	41	19	AAV51081	Maize polymorphic	c 783	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 711	13.2	14.2	41	19	AAV51081	Maize polymorphic	c 784	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 712	13.2	14.2	41	19	AAV47838	Maize polymorphic	c 785	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 713	13.2	14.2	41	19	AAV47838	Maize polymorphic	c 786	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 714	13.2	14.2	41	24	AB156720	Probes #2 for huma	c 787	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 715	13.2	14.2	41	24	ABK50237	Setline/chreonine k	c 788	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 716	13.2	14.2	41	24	ABK50238	Human motor protei	c 789	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 717	13.2	14.2	41	24	ABK50285	Human alpha 2,3-si	c 790	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 718	13.2	14.2	41	24	AB142407	Human LAR protein	c 791	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 719	13.2	14.2	41	24	AB152984	Primer used in con	c 792	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 720	13.2	14.2	42	20	AAV72567	B. licheniformis a	c 793	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 721	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 794	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 722	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 795	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 723	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 796	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 724	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 797	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 725	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 798	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 726	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 799	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 727	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 800	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 728	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 801	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 729	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 802	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 730	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 803	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 731	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 804	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 732	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 805	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 733	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 806	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 734	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 807	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 735	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 808	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 736	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 809	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 737	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 810	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 738	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 811	13.2	14.2	50	22	AA133686	Human SNP oligonuc
c 739	13.2	14.2	42	20	AAV72567	Sendai virus M-F s	c 812	13.2	14.2	50	22	AA133686	Human SNP oligonuc

C 813	13	14.0	26	22	AA51314	Human NOV4 RTG PCR	C 886	13	14.0	40	18	AA87125	IFN-gamma 2' RNA
C 814	13	14.0	26	24	AA39016	Human mtr1 gene HI	C 887	13	14.0	40	19	AA330086	Primer used to fus
C 815	13	14.0	26	24	AA32652	Human ACE-2 exon 1	C 888	13	14.0	40	19	AA330087	Primer used to fus
C 816	13	14.0	27	22	AAH39439	SNP specific SNPE	C 889	13	14.0	40	20	AA28716	Oligonucleotide Na
C 817	13	14.0	27	24	AAH40828	Oligo relating to	C 890	13	14.0	40	21	AA281624	Escherichia coli r
C 818	13	14.0	27	24	ABK6830	Prelyl diposphatase	C 891	13	14.0	40	21	AA501067	PCR primer ZC18149
C 819	13	14.0	28	17	AA39046	Antisense primer #	C 892	13	14.0	40	21	AA521344	Mutated TB82 prime
C 820	13	14.0	28	17	AA31342	CCR-3 receptor nes	C 893	13	14.0	40	21	AA48410	Primer specific fo
C 821	13	14.0	28	22	AA30574	Human Factor V gen	C 894	13	14.0	40	21	AA440131	Capture extender p
C 822	13	14.0	29	14	AA042374	TBD3 promoter 5'p	C 895	13	14.0	40	21	AA420273	Capture probe #d41
C 823	13	14.0	29	19	AAV08792	PCR primer TDH3-5'	C 896	13	14.0	40	22	AA21265	HBVcore phosphora
C 824	13	14.0	29	21	AA28682	Human ADAM DNA PCR	C 897	13	14.0	40	22	AA330152	Capture extender p
C 825	13	14.0	29	22	AAH75011	Probe for human TA	C 898	13	14.0	40	24	AB158595	Oligonucleotide MO
C 826	13	14.0	29	22	AAH75011	Primer #7. Uniden	C 899	13	14.0	40	24	AB159213	Green/red click be
C 827	13	14.0	29	24	AAH31436	Yeast TDH3 promote	C 900	13	14.0	40	24	AB159303	Synthetic Renilla
C 828	13	14.0	29	24	AA28016	Human T-cell recep	C 901	13	14.0	40	24	ABA92143	Corynebacterium q1
C 829	13	14.0	30	20	AA336975	Human cd37 nuclel	C 902	13	14.0	40	24	ABK14053	Porin expression r
C 830	13	14.0	30	20	AA336975	Streptococcus dysg	C 903	13	14.0	41	19	AAV47718	Maize polymorphic
C 831	13	14.0	31	13	AA022076	Sequence of primer	C 904	13	14.0	41	22	AAH45527	Human deafness rel
C 832	13	14.0	31	13	AA028913	PCR primer DG284 f	C 905	13	14.0	41	22	AAH57505	TOLA gene amplifit
C 833	13	14.0	31	18	AA80527	Alcohol oxidase ge	C 906	13	14.0	41	22	AA02582	Forward primer #2
C 834	13	14.0	31	19	AAV67758	Nucleotide fragmen	C 907	13	14.0	41	24	AB159208	Human tyrosinase 1
C 835	13	14.0	31	24	AA636252	ISAV 9AI cDNA clon	C 908	13	14.0	42	19	AAV50745	Brassica sp. polyM
C 836	13	14.0	31	24	ABK65050	Human gene specific	C 909	13	14.0	42	19	AAV47880	Maize polymorphic
C 837	13	14.0	32	18	AA60551	Progestin regulate	C 910	13	14.0	42	21	AA673347	Single base extens
C 838	13	14.0	32	18	AA745811	Glucocorticoid rec	C 911	13	14.0	42	21	AA559403	DNA encoding a con
C 839	13	14.0	32	19	AA788332	Antisense oligonuc	C 912	13	14.0	42	21	AA87263	PCR primer used to
C 840	13	14.0	33	17	AA742604	Primer #8 for rece	C 913	13	14.0	42	22	AAH77723	Brassica polymorph
C 841	13	14.0	33	17	AA742604	Primer used in rec	C 914	13	14.0	42	24	AB159104	Spinocerbellar at
C 842	13	14.0	33	17	AA727055	5'-Primer for HIS3	C 915	13	14.0	43	16	AA084801	Sense primer for s
C 843	13	14.0	33	18	AA710186	Human immunoglobul	C 916	13	14.0	43	17	AA736014	Plasmids pVMSOSIB
C 844	13	14.0	33	18	AA710186	Primer #8 for huma	C 917	13	14.0	43	19	AAV33648	Gy2 element core s
C 845	13	14.0	33	19	AAV51598	Human IgG1p PCR p	C 918	13	14.0	43	20	AAV72265	Antibody kappa cha
C 846	13	14.0	33	19	AAV51598	Human B7.1 cDNA 5'	C 919	13	14.0	43	20	AAV70670	PCR primer OH3-2pr
C 847	13	14.0	33	20	AA116826	Human delta-1 gene	C 920	13	14.0	43	17	AA734718	PCR primer OPR132
C 848	13	14.0	33	20	AA116826	Human delta-2 prim	C 921	13	14.0	44	18	AA794801	Forward primer for
C 849	13	14.0	33	23	AB155920	Human BPTL x PCR p	C 922	13	14.0	44	18	AA794801	Primer used in MHC
C 850	13	14.0	33	24	AB152981	Human LAR protein	C 923	13	14.0	44	18	AA794801	Primer used in MHC
C 851	13	14.0	33	24	ABA92304	Human microtubule	C 924	13	14.0	44	18	AA794801	Primer used in MHC
C 852	13	14.0	34	16	AA151374	AZF ASF cosmid clo	C 925	13	14.0	45	16	AA705745	Endonuclease stran
C 853	13	14.0	34	17	AA728043	Ribozyme analogue	C 926	13	14.0	45	17	AA728306	Primer NP4 used in
C 854	13	14.0	34	22	AA508269	Human GPCR, htrp13	C 927	13	14.0	45	19	AAV54495	Linker primer L15D
C 855	13	14.0	34	24	AB157081	Human interleukin-	C 928	13	14.0	45	19	AAV44557	Primer L15D for hu
C 856	13	14.0	35	20	AA225388	Infectious pancrea	C 929	13	14.0	45	21	AA665116	PCR primer #3n+tr
C 857	13	14.0	35	20	AA225400	Infectious pancrea	C 930	13	14.0	46	21	AA665116	EGFP effector sequ
C 858	13	14.0	35	20	AA225400	Oligonucleotide pr	C 931	13	14.0	46	21	AA665116	Maize CROBS/5PC-01
C 859	13	14.0	35	21	AAK9186	3' PCR primer of T	C 932	13	14.0	46	21	AA665116	Primer CROBS/5PC-01
C 860	13	14.0	35	22	AA170038	Tag DNA polymerase	C 933	13	14.0	47	19	AA665116	Penicillium chrysos
C 861	13	14.0	36	18	AAV1787	Human colon specif	C 934	13	14.0	47	21	AA665116	Human map-related
C 862	13	14.0	36	19	AAV1984	C3-degrading prote	C 935	13	14.0	47	21	AA665116	Human map-related
C 863	13	14.0	36	20	AAK03198	5' PCR primer prim	C 936	13	14.0	47	21	AA665116	Human map-related
C 864	13	14.0	36	21	AAK03198	PCR primer for amp	C 937	13	14.0	47	21	AA665116	Human map-related
C 865	13	14.0	37	17	AA738273	Murine 200 gene fo	C 938	13	14.0	47	21	AA665116	Human map-related
C 866	13	14.0	37	20	AAV70972	Oligonucleotide ND	C 939	13	14.0	47	21	AA665116	Human map-related
C 867	13	14.0	37	21	ABA96827	Human parathyroid	C 940	13	14.0	47	21	AA665116	Human map-related
C 868	13	14.0	37	21	AAV1906	Forward primer for	C 941	13	14.0	47	21	AA665116	Human map-related
C 869	13	14.0	37	22	AA170269	Mouse 200 gene for	C 942	13	14.0	47	21	AA665116	Human map-related
C 870	13	14.0	37	22	AA170269	Murine thl specifl	C 943	13	14.0	47	21	AA665116	Human map-related
C 871	13	14.0	37	22	AA690994	Mouse 200 gene PCR	C 944	13	14.0	47	21	AA665116	Human map-related
C 872	13	14.0	37	22	AA690994	Forward oligonucle	C 945	13	14.0	47	21	AA665116	Human map-related
C 873	13	14.0	38	19	AAV07069	Degenerate probe f	C 946	13	14.0	48	14	AA040933	Probe p255. Synth
C 874	13	14.0	38	21	AAZ54759	Neisseria species	C 947	13	14.0	48	14	AA040933	HIV gag INS mutage
C 875	13	14.0	38	23	ABK04702	Human NCOG Inozyme	C 948	13	14.0	48	16	AA050226	NLS reverse primer
C 876	13	14.0	38	23	ABK05331	Human NCOG Inozyme	C 949	13	14.0	48	19	AA050226	A. cellulolyticus
C 877	13	14.0	38	23	ABK05892	Human NCOG Inozyme	C 950	13	14.0	48	19	AA050226	A. cellulolyticus
C 878	13	14.0	39	17	AA10143	Sense primer for C	C 951	13	14.0	48	21	AAV57674	PCR primer for det
C 879	13	14.0	39	17	AA11562	Murine Fas antigen	C 952	13	14.0	49	15	AA070149	Example of oligonu
C 880	13	14.0	39	19	AAV55501	Flt-3 receptor ago	C 953	13	14.0	50	17	AA070149	Template oligonuc
C 881	13	14.0	39	19	AAV44563	Primer 339REV3 for	C 954	13	14.0	50	17	AA070149	Model sequence use
C 882	13	14.0	39	22	AAV27922	Human IL-1IL codin	C 955	13	14.0	50	19	AA190058	Probe used to iso
C 883	13	14.0	40	16	AA089131	Nucleic acid ligan	C 956	13	14.0	50	20	AA190058	Synthetic oligonuc
C 884	13	14.0	40	18	AA798478	Interleukin-10 2'f	C 957	13	14.0	50	22	AA190058	Human SNP oligonuc
C 885	13	14.0	40	18	AA798478	Interleukin-10 2'f	C 958	13	14.0	50	22	AA190058	Human SNP oligonuc

C 959 13 14.0 50 22 AAL29177 Human SNP oligonuc
 C 960 13 14.0 50 22 AAL31470 Human SNP oligonuc
 C 961 13 14.0 50 22 AAL33774 Human SNP oligonuc
 C 962 13 14.0 50 22 AAL33914 Human SNP oligonuc
 C 963 13 14.0 50 22 AAL33915 Human SNP oligonuc
 C 964 13 14.0 50 22 AAL34488 Human SNP oligonuc
 C 965 13 14.0 50 22 AAL75281 Human silent SNP c
 C 966 13 14.0 50 22 AAL44112 50-mer oligonucleo
 C 967 13 14.0 50 22 AAF72515 Human PRO polypept
 C 968 13 14.0 50 22 AAF61742 TMV 54k protein ma
 C 969 13 14.0 50 24 AAS17560 MOKIV envelope gly
 C 970 12.8 13.8 17 21 AAB7041 Probe to Alu2 huma
 C 971 12.8 13.8 17 22 AAB5562 Human CHX1 ribozym
 C 972 12.8 13.8 17 22 AAB7282 Human CICAL gene e
 C 973 12.8 13.8 19 16 AAO82623 Chromosome 11 (loc
 C 974 12.8 13.8 19 19 AAV57826 Human chromosome 1
 C 975 12.8 13.8 19 22 ABA82416 Zmax1 gene region
 C 976 12.8 13.8 19 24 ABR6705 Interleukin-3 (IL-
 C 977 12.8 13.8 19 24 ABR23213 Human zmax1 cDNA f
 C 978 12.8 13.8 20 16 AAT41198 Human gene signatu
 C 979 12.8 13.8 20 16 AAO98959 Human 12-11poxigen
 C 980 12.8 13.8 20 20 AAZ03218 PCR primer used to
 C 981 12.8 13.8 20 20 AAB5551 PCR primer used to
 C 982 12.8 13.8 20 21 AAZ75627 Human ballelic ma
 C 983 12.8 13.8 20 21 AAC72296 Single nucleotide
 C 984 12.8 13.8 20 21 AAC72311 Single nucleotide
 C 985 12.8 13.8 20 21 AAC72320 Single nucleotide
 C 986 12.8 13.8 20 21 AAM11892 Human MDMX antisen
 C 987 12.8 13.8 20 21 AAM11935 Human MDMX antisen
 C 988 12.8 13.8 20 21 AAM11941 Human MDMX antisen
 C 989 12.8 13.8 20 24 ABR194620 Capture oligonucle
 C 990 12.8 13.8 21 20 AAZ28414 PCR primer UDS2160
 C 991 12.8 13.8 21 20 AAV45595 Primer for 3' end
 C 992 12.8 13.8 21 21 AAV97198 A. thaliana NIM1 h
 C 993 12.8 13.8 21 17 AAT74038 Reverse PCR primer
 C 994 12.8 13.8 22 17 AAT38270 Murine gamma actin
 C 995 12.8 13.8 22 17 AAT36056 Gamma-actin forar
 C 996 12.8 13.8 22 20 AAY26252 Reverse primer for
 C 997 12.8 13.8 22 20 AAY81832 Mouse gamma-actin
 C 998 12.8 13.8 22 21 AAG61615 Mismatch probe spe
 C 999 12.8 13.8 22 21 AAG61620 Mismatch probe spe
 C1000 12.8 13.8 22 21 AAB8589 PCR primer for mou

ALIGNMENTS

RESULT 1

ID AAC90373 standard; DNA: 43 BP.
 AC AAC90373;

DT 19-MAR-2001 (first entry)
 DE PF1ag-CMV-5a:METH1 PCR primer #2.

METH1: metalloprotease; thrombospondin; angiogenesis inhibition;
 cancer therapy; benign tumour; ocular angiogenic disease; PCR primer;
 rheumatoid arthritis; psoriasis; wound healing; endometriosis;
 vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
 scleroderma; trachoma; vascular adhesions; myocardial angiogenesis;
 coronary collateral; cerebral collateral; arteriovenous malformation;
 ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;
 plaque neovascularisation; telangiectasia; haemophilic joint; EST;
 angiodioma; fibromuscular dysplasia; expressed sequence tag;
 Crohn's disease; atherosclerosis; birth control; ss.

OS Homo sapiens.
 XX
 PN WO200071577-A1.
 XX
 PD 30-NEW-2000.

XX 25-MAY-2000; 2000MC-US14462.
 PF 25-MAY-1999; 9905-0318208.
 XX 20-JUL-1999; 9905-0144882.
 PR 10-AUG-1999; 9905-0147823.
 PR 13-AUG-1999; 9905-0373658.
 PR 22-DEC-1999; 9905-0171503.
 PR 22-FEB-2000; 2000US-0183792.
 XX (HWA-) HUMAN GENOME SCI INC.
 PA (SMK-) SMITHKLINE BEECHAM CORP.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (IRUE-) IRUELA-ARISPE L.
 PA (HAST-) HASTINGS G A.
 PA (RUBE-) RUBEN S M.
 PA (JONAK-) JONAK Z L.
 PA (TRULL-) TRULLI S H.
 PA (FORN-) FORNARD J A.
 PA (TERRE-) TERRETT J A.
 XX Truella-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trullli SH;
 PI Fornwald JA, Terrett JA;
 PI WPI: 2001-025136/03.
 XX METH1 and METH2 polynucleotides and encoded polypeptides, used to
 PT inhibit angiogenesis in the treatment of disorders such as cancer,
 PT rheumatoid arthritis and psoriasis -
 XX Example 52; Page 478; 768pp; English.
 PS The present invention relates to human METH1 and METH2, (ME for
 CC metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).
 CC The present sequence is a PCR primer used in the present invention. METH
 CC can be used for inhibiting angiogenesis in an individual, and for
 CC treating cancer, benign tumours, an ocular angiogenic disease,
 CC rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis,
 CC vasculogenesis, granulations, hypertrophic scars, nonunion fractures,
 CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
 CC coronary collateral, cerebral collateral, arteriovenous malformations,
 CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,
 CC fibromuscular dysplasia, wound granulation, Crohn's disease or
 CC atherosclerosis. METH can also be used in birth control. METH can also
 CC be used in diagnostic methods for the prognosis of cancer.
 CC
 XX Sequence 43 BP; 10 A; 11 C; 10 G; 12 T; 0 other;

Query Match 19.4%; Score 18; DB 22; Length 43;
 Best Local Similarity 70.6%; Pred. No. 3; Be+03;
 Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 GGAGCACTCCATTCTGCTGGGTGACAAAGCCT 39
 DB 7 GGTACCACTGCAATTCCTGCTGCAAAAGCTCA 40

RESULT 2

ID AAN80618 standard; DNA: 32 BP.
 AC AAN80618;

DT 08-OCT-1990 (first entry)
 DE Probe (32n) for the detection Bovine Bone Morphogenic Protein-1 sequence.

METH1: metalloprotease; thrombospondin; angiogenesis inhibition;
 cancer therapy; benign tumour; ocular angiogenic disease; PCR primer;
 rheumatoid arthritis; psoriasis; wound healing; endometriosis;
 vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
 scleroderma; trachoma; vascular adhesions; myocardial angiogenesis;
 coronary collateral; cerebral collateral; arteriovenous malformation;
 ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;
 plaque neovascularisation; telangiectasia; haemophilic joint; EST;
 angiodioma; fibromuscular dysplasia; expressed sequence tag;
 Crohn's disease; atherosclerosis; birth control; ss.

XX	PN	WO8800205-A.	
XX	PD	14-JAN-1988.	
XX	PF	30-JUN-1987; 87WO-US01537.	
XX	PR	26-MAR-1987; 87US-0031346.	
XX	PA	(GENE-) GENETICS INST INC.	
XX	PI	Wozney JM, Rosen VA;	
XX	DR	WPI; 1988-021565/03.	
XX	PT	Bone morphogenic proteins - obd. using recombinant DNA and used	
XX	PT	for inducing cartilage and bone formation.	
XX	PS	Disclosure; ; 7pp: English.	
XX	CC	This probe is a relatively long (32 nucleotides) "guesser" [See	
XX	CC	J.J. Toole et al, Nature, 312:342-347 (1984)]. The regions of the amino	
XX	CC	acid sequence used for probe design are chosen by avoiding highly	
XX	CC	degenerate codons where possible. The probe is radiolabelled with	
CC	CC	polynucleotide kinase and 32P-gamma-ATP and used to screen a bovine cDNA	
CC	CC	library.	
CC	CC	See also AAN80619-N80636 and AAN81963-64.	
XX	SO	Sequence 32 BP; 7 A; 11 C; 9 G; 5 T; 0 other;	
XX	SO	Query Match 18.38; Score 17; DB 9; Length 32;	
		Best Local Similarity 80.0%; Pred. No. 8.1e+03;	
		Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Oy		20 CTGCCTGGGTGACATGCGTGGTT 44	
Db		30 CTCTCTGGCGACATCTGCCCTGGAT 6	
RESULT 3			
AAL45727			
ID		AAL45727 standard; DNA; 49 BP.	
AC		AAL45727;	
XX	DT	27-JUN-2002 (first entry)	
XX	DE	Cancer cells detection oligonucleotide A18-1.	
XX	DE	Cancer; extranuclear DNA; stem-loop; DNA-binding protein; cytosolic;	
KW	XX	tumour cell detection; ss.	
OS	XX	Homo sapiens.	
PH	Key	Location/Qualifiers	
FT	FT	6..10	
FT	FT	/tag= a	
FT	FT	/bound_molety= "nucleotides 44-40 of itself"	
FT	FT	12	
FT	FT	/tag= b	
FT	FT	/bound_molety= "nucleotide 38 of itself"	
FT	FT	14..15	
FT	FT	/tag= c	
FT	FT	/bound_molety= "nucleotides 36-35 of itself"	
FT	FT	17..19	
FT	FT	/tag= d	
FT	FT	/bound_molety= "nucleotides 33-31 of itself"	
FT	FT	21..23	
FT	FT	/tag= e	
FT	FT	/bound_molety= "nucleotides 29-27 of itself"	
FT	FT	27..33	
FT	FT	/tag= f	
FT	FT	/bound_molety= "NKX2.5"	
FT	FT	27..29	
FT	FT	misc_binding	

FT	misc_binding	18.38	Score 17: DB 24: Length 49:	Query Match	Best Local Similarity 63.48; Pred No. 9.3e+03;	Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0
FT	misc_binding	31.33	/*tag= 9	DE10046318-A1.	28-MAR-2002.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	35.36	/bound_molecy= "nucleotides 23-21 of itself"	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	35.36	/*tag= h	(ABKE/) ABKEN H.	Abken H, Schinkoethe T;	WPI: 2002-331116/37.
FT	misc_binding	38	/bound_molecy= "nucleotides 19-17 of itself"	Claim 21: Page 10; 27pp; German.	Detecting tumor cells from presence of specific stem-loop DNA molecules outside the nucleus, useful for diagnosis and monitoring of tumors -	Claim 21: Page 10; 27pp; German.
FT	misc_binding	38	/*tag= i	The present invention relates to a method of detecting tumour cells, by detecting extranuclear DNA consisting of a single-strand with a double-stranded stem-loop structure containing at least 2 binding sites for DNA binding proteins. The method can be used to detect cancer cells in tissue sections, biopsies, body fluids etc, and can be used in the diagnosis and monitoring of cancer. The present sequence is an extranuclear DNA sequence capable of being detected using the method of the invention.	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;
FT	misc_binding	38	/bound_molecy= "nucleotides 15-14 of itself"	Query Match	Best Local Similarity 63.48; Pred No. 9.3e+03;	Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0
FT	misc_binding	38	/*tag= j	DE10046318-A1.	28-MAR-2002.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/bound_molecy= "nucleotide 12 of itself"	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/*tag= k	(ABKE/) ABKEN H.	Abken H, Schinkoethe T;	WPI: 2002-331116/37.
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Claim 21: Page 10; 27pp; German.	Detecting tumor cells from presence of specific stem-loop DNA molecules outside the nucleus, useful for diagnosis and monitoring of tumors -	Claim 21: Page 10; 27pp; German.
FT	misc_binding	38	/*tag= k	The present invention relates to a method of detecting tumour cells, by detecting extranuclear DNA consisting of a single-strand with a double-stranded stem-loop structure containing at least 2 binding sites for DNA binding proteins. The method can be used to detect cancer cells in tissue sections, biopsies, body fluids etc, and can be used in the diagnosis and monitoring of cancer. The present sequence is an extranuclear DNA sequence capable of being detected using the method of the invention.	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Query Match	Best Local Similarity 63.48; Pred No. 9.3e+03;	Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0
FT	misc_binding	38	/*tag= k	DE10046318-A1.	28-MAR-2002.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/bound_molecy= "nucleotide 12 of itself"	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/*tag= k	(ABKE/) ABKEN H.	Abken H, Schinkoethe T;	WPI: 2002-331116/37.
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Claim 21: Page 10; 27pp; German.	Detecting tumor cells from presence of specific stem-loop DNA molecules outside the nucleus, useful for diagnosis and monitoring of tumors -	Claim 21: Page 10; 27pp; German.
FT	misc_binding	38	/*tag= k	The present invention relates to a method of detecting tumour cells, by detecting extranuclear DNA consisting of a single-strand with a double-stranded stem-loop structure containing at least 2 binding sites for DNA binding proteins. The method can be used to detect cancer cells in tissue sections, biopsies, body fluids etc, and can be used in the diagnosis and monitoring of cancer. The present sequence is an extranuclear DNA sequence capable of being detected using the method of the invention.	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Query Match	Best Local Similarity 63.48; Pred No. 9.3e+03;	Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0
FT	misc_binding	38	/*tag= k	DE10046318-A1.	28-MAR-2002.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/bound_molecy= "nucleotide 12 of itself"	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/*tag= k	(ABKE/) ABKEN H.	Abken H, Schinkoethe T;	WPI: 2002-331116/37.
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Claim 21: Page 10; 27pp; German.	Detecting tumor cells from presence of specific stem-loop DNA molecules outside the nucleus, useful for diagnosis and monitoring of tumors -	Claim 21: Page 10; 27pp; German.
FT	misc_binding	38	/*tag= k	The present invention relates to a method of detecting tumour cells, by detecting extranuclear DNA consisting of a single-strand with a double-stranded stem-loop structure containing at least 2 binding sites for DNA binding proteins. The method can be used to detect cancer cells in tissue sections, biopsies, body fluids etc, and can be used in the diagnosis and monitoring of cancer. The present sequence is an extranuclear DNA sequence capable of being detected using the method of the invention.	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Query Match	Best Local Similarity 63.48; Pred No. 9.3e+03;	Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0
FT	misc_binding	38	/*tag= k	DE10046318-A1.	28-MAR-2002.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/bound_molecy= "nucleotide 12 of itself"	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/*tag= k	(ABKE/) ABKEN H.	Abken H, Schinkoethe T;	WPI: 2002-331116/37.
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Claim 21: Page 10; 27pp; German.	Detecting tumor cells from presence of specific stem-loop DNA molecules outside the nucleus, useful for diagnosis and monitoring of tumors -	Claim 21: Page 10; 27pp; German.
FT	misc_binding	38	/*tag= k	The present invention relates to a method of detecting tumour cells, by detecting extranuclear DNA consisting of a single-strand with a double-stranded stem-loop structure containing at least 2 binding sites for DNA binding proteins. The method can be used to detect cancer cells in tissue sections, biopsies, body fluids etc, and can be used in the diagnosis and monitoring of cancer. The present sequence is an extranuclear DNA sequence capable of being detected using the method of the invention.	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;	Sequence 49 BP; 12 A; 8 C; 11 G; 18 T; 0 other;
FT	misc_binding	38	/bound_molecy= "nucleotides 10-6 of itself"	Query Match	Best Local Similarity 63.48; Pred No. 9.3e+03;	Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0
FT	misc_binding	38	/*tag= k	DE10046318-A1.	28-MAR-2002.	19-SEP-2000; 2000DE-1046318.
FT	misc_binding	38	/bound_molecy= "nucleotide 12 of itself"	19-SEP-2000; 2000DE-1046318.	19-SEP-2000; 2000DE	


```

CC the construction of herpesvirus expression vectors.
XX
SQ Sequence 33 BP; 8 A; 9 C; 11 G; 5 T; 0 other:
Query Match 17.8%; Score 16.6; DB 21; Length 33;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 64 ACTGTCGGGCGCTCCGAAACAT 86
1 | | | | | | | | | | | | | | | | | |
10 AATGTCGGGCGCTCCGAAACAT 32

RESULT 7
AAT08201/c
ID AAT08201 standard; DNA; 39 BP.
XX
AC AAT08201;
XX
DT 28-MAY-1996 (first entry)
XX
DE Amplification primer BK138.
XX
KW Linker; interleukin-4; interleukin-2; IL-4; IL-2; G-CSF; GM-CSF;
KW granulocyte-colony stimulating factor; circularly permuted ligand;
KW cancer; granulocyte macrophage-colony stimulating factor;
KW polymerase chain reaction; PCR; primer; amplify; ss.
XX
OS Synthetic.
XX
PN WO9527732-A2.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US04468.
XX
PR 08-APR-1994; 94US-0225224.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kretzman RJ, Pastan I;
XX
DR WPI; 1995-366354/47.
XX
PT Circularly permuted ligands and chimeric mols. are modified
PT interleukin(s) or colony-stimulating factors - with increased
PT binding specificity and affinity for inhibiting tumours
XX
PS Example 5; Page 35; 97pp; English.
XX
CC AAT08176-T08219 represent amplification primers used in the construction
CC of modified ligands. The modified ligands comprise two copies of a
CC sequence joined to a linker. The sequences used in the ligand include
CC interleukin-4 (IL-4), IL-2, granulocyte-colony stimulating factor
CC (G-CSF) and granulocyte macrophage-colony stimulating factor (GM-CSF).
CC The linker regions used are represented by AAR87726 and AAR87730. This
CC sequence was used in conjunction with AAT08200 to amplify codons 39-127
CC of IL-2 for use in a modified ligand. These modified ligands are known
CC as circularly permuted ligands. The modified ligands can be joined to
CC another protein (preferably a cytotoxin or an antibody) using a spacer
CC (see AAR87732-R87734). The circularly permuted ligands have greater
CC specificity and binding affinity than the original ligand. They can be
CC used in chimeric molecules to inhibit the growth of tumour cells in vivo,
CC where the two copies of the protein sequence are joined to cytotoxins.
XX
SQ Sequence 39 BP; 7 A; 10 C; 12 G; 10 T; 0 other:
Query Match 17.8%; Score 16.6; DB 16; Length 39;
Best Local Similarity 71.0%; Pred. No. 1.2e+04;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 43 TTTCACACTATCGAATGCTGCTGGGC 73
1 | | | | | | | | | | | | | | | | | |

DB 35 TCTCAACACTCACCGAGGTAACGGTGGGC 5
RESULT 8
AAC90375
ID AAC90375 standard; DNA; 43 BP.
XX
AC AAC90375;
XX
DT 19-MAR-2001 (first entry)
XX
DE pCAFc:METH1 PCR primer #2.
XX
KW METH1: metalloproteinase; thrombospondin; angiogenesis inhibition;
KW cancer therapy; benign tumour; ocular angiogenic disease; PCR primer;
KW rheumatoid arthritis; psoriasis; wound healing; endometriosis;
KW vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
KW scleroderma; trachoma; vascular adhesion; myocardial angiogenesis;
KW coronary collateral; cerebral collateral; arteriovenous malformation;
KW ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;
KW plaque neovascularisation; telangiectasia; haemophilic joint; EST;
KW angiofibroma; fibromuscular dysplasia; expressed sequence tag;
KW Crohn's disease; atherosclerosis; birth control; ss.
XX
OS Homo sapiens.
XX
PN WO200071577-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-2000; 2000WO-US14462.
XX
PR 20-JUL-1999; 99US-0318208.
PR 10-AUG-1999; 99US-0144882.
PR 13-AUG-1999; 99US-0147823.
PR 22-DEC-1999; 99US-0373638.
PR 22-FEB-2000; 2000US-0183792.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIT) SMITHKLINE BEECHAM CORP.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA (TRUE/) TRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
PA (JONA/) JONAK Z L.
PA (TRUL/) TRULLI S H.
PA (FORN/) FORMALD J A.
PA (TERR/) TERRETT J A.
XX
PI Truella-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trull SH;
PI FORMALD JA, Terrett JA;
XX
DR WPI; 2001-025136/03.
XX
PT METH1 and METH2 polynucleotides and encoded polypeptides, used to
PT inhibit angiogenesis in the treatment of disorders such as cancer,
PT rheumatoid arthritis and psoriasis -
XX
PS Example 52; Page 479; 768pp; English.
XX
CC The present invention relates to human METH1 and METH2, (ME for
CC metalloproteinase and TH for thrombospondin; see AAB50002 and AAB50003)
CC The present sequence is a PCR primer used in the present invention. METH
CC can be used for inhibiting angiogenesis in an individual, and for
CC treating cancer, benign tumours, an ocular angiogenic disease,
CC rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis,
CC vasculogenesis, granulations, hypertrophic scars, nonunion fractures,
CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
CC coronary collaterals, cerebral collateral, arteriovenous malformations,
CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC fibromuscular dysplasia, wound granulation, Crohn's disease or

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XX 21-APR-1999; 99WO-IB00822.
 PF 21-APR-1998; 98US-0082614.
 PR 23-NOV-1998; 98US-0109732.
 XX (GEST) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI WPI: 2000-013267/01.
 DR
 XX Novel diallelic markers used to construct a high density disequilibrium
 PT map of the human genome
 XX
 PS Claim 1; Page 540; 2745pp; English.
 CC AA265654 to AA269578 represent human diallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the diallelic markers. The diallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.
 CC
 SQ Sequence 47 BP; 16 A; 6 C; 16 G; 9 T; 0 other;
 Query Match 17.6%; Score 16.4; DB 21; Length 47;
 Best Local Similarity 67.6%; Pred. No. 1.5e+04;
 Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 20 CTGCTGGGTGACATGCGCTTGGTTCACTCACTA 53
 Db 36 CTGCTTCTCCTACGTATGCTTGGTTTCCATCTCA 3
 RESULT 16
 AAL34180
 ID AAL34180 standard; DNA; 50 BP.
 XX
 AC AAL34180;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #7388.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; cholesteryl; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 PI Shimkets RA, Leach M;
 XX
 DR WPI: 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections
 XX
 PS Claim 1; Page 3513; 4143pp; English.
 CC
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and cholesterylases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 SQ Sequence 50 BP; 10 A; 17 C; 20 G; 3 T; 0 other;
 Query Match 17.6%; Score 16.4; DB 22; Length 50;
 Best Local Similarity 67.6%; Pred. No. 1.6e+04;
 Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 55 CGGATGTGACTGTCGGCCTCCAGAAACATTG 88
 Db 17 CGGAGCGCGCCGAGCGGCTCCCAAAAGCCTG 50
 RESULT 17
 AAT75539
 ID AAT75539 standard; DNA; 50 BP.
 XX
 AC AAT75539;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:2480.
 XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US32758.
 XX
 PR 30-NOV-1999; 99US-0168138.
 XX
 PR 29-NOV-2000; 2000US-0726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI: 2001-356160/37.
 XX

5'-ends of mRNA molecules. It allows the production of cDNA libraries from nanogram quantities of total or polyA+ RNA.

Sequence 40 BP; 12 A; 9 C; 16 G; 3 T; 0 other;

Query Match 17.4%; Score 16.2; DB 20; Length 40;
Best Local Similarity 64.9%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

3 GCTGGAGCACTCCATTCCTGCTGGTACATGCTT 39
Db 37 GCTGGTCTGCTGCCACTCTGCTGTATACACTGCTT 1

RESULT 20

AAV76941/c
ID AAV76941 standard; DNA; 50 BP.

AAV76941;

16-MAR-1999 (first entry)

Staphylococcus aureus contig SEQ ID #2630.

Computer readable medium; vaccine; S.aureus infection; immunodetection;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome; ds.

Staphylococcus aureus.

EP766519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-0100117.

05-JAN-1996; 96US-0009861.

(HUMAN-) HUMAN GENOME SCI INC.

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus
stored on computer readable medium and used in the production of
anti-S.aureus vaccines

Claim 1; Page 2293; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

Sequence 50 BP; 16 A; 10 C; 14 G; 9 T; 1 other;

Query Match 17.4%; Score 16.2; DB 18; Length 50;
Best Local Similarity 72.4%; Pred. No. 1.9e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

37 CCTTGTTTCAACACATGCAATGTGAC 65
Db 47 CTTTGTTTAAACCAATGCGCTTTAAC 19

RESULT 21

AA27838
ID AA27838 standard; DNA; 50 BP.

AA27838;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #1046.

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
neutroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
amyloid protein; angiotensin; apoptosis related protein; cadherin;
cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
complement related protein; cytochrome; kinase; cytokine; interferon;
interleukin; G-protein coupled receptor; thioesterase; inflammation;
multifactorial disease; autoimmune disease; infection;
nervous system disease; ss.

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

Claim 1; Page 1679; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 50 BP; 20 A; 7 C; 5 G; 18 T; 0 other;

Query Match 17.4%; Score 16.2; DB 22; Length 50;
Best Local Similarity 64.9%; Pred. No. 1.9e+04;
Matches 24; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

XX MPI; 2001-465210/50.

XX polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections -

PS Claim 1; Page 3446; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms.

SQ Sequence 50 BP; 9 A; 21 C; 12 G; 8 T; 0 other;

Query Match

Best Local Similarity 17.2%; Score 16; DB 22; Length 50;

Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 41 GGTTCACACTATCGAATGACATGTCGGGCTCCAGA 80
II IIIIIII I IIIIIII IIIIIII IIIIIII
DB 49 GCGACGACGACCTGTGTAGGTGCTGACGCTCCAGCGA 10

RESULT 27

ID AAH89751/C

AAH89751 standard; DNA; 50 BP.

XX AAH89751;

DT 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 532.

XX Human; single nucleotide polymorphism; SNP; paternity test;
XX forensic test; aberrant protein expression; ds.

OS Homo sapiens.

XX WO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach MD;

XX WPI; 2001-451871/48.

XX P-PSDB; AAM00634.

XX Isolated human polynucleotides containing single nucleotide
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX infection and diabetes -

XX Claim 1; Page 257; 475pp; English.

CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.

SQ Sequence 50 BP; 13 A; 18 C; 14 G; 5 T; 0 other;

Query Match

Best Local Similarity 17.2%; Score 16; DB 22; Length 50;

Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 21 TGCCGTGGTGACATGCCCTTGTTCCACACT 52
IIIIIIII I IIIIIII IIIIIII IIIIIII
DB 43 TGCCGTGGCGGCTGTGCCACAGTTCTCCAGT 12

RESULT 28

ID AAV63698/C

AAV63698 standard; DNA; 35 BP.

XX AAV63698;

DT 11-MAR-1999 (first entry)

XX PCR primer used to amplify HIV-2 sequences.

XX HIV-1, HIV-2; detection; Acquired Immunodeficiency Syndrome; AIDS;
XX co-amplification assay; PCR primer; ss.

XX Synthetic.

XX Human immunodeficiency virus type 2.

XX EP887427-A2.

XX 30-DEC-1998.

XX 24-JUN-1998; 98EP-0304959.

XX 25-JUN-1997; 97US-0050759.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX Atwood SM, Backus JW, Casey AE, Cummins TJ, Rasmussen EB;

XX WPI; 1999-047891/05.

XX Detecting Human Immunodeficiency Virus 1 and 2 - using at least
XX four new oligonucleotide primers and multiple detection probes

XX Disclosure; Page 11; 25pp; English.

XX The present PCR primer is used to amplify human deficiency type 2
XX (HIV-2) nucleic acids. The specification also describes primers and
XX probes for HIV-1 and HIV-2. The primers and probes are useful for
XX amplifying and detecting HIV-1 and HIV-2 and all their subtype nucleic
XX acids in biological samples, and for giving progress in our
XX understanding of Acquired Immunodeficiency Syndrome (AIDS). The primers
XX are able to detect all HIV-1 and HIV-2 subtypes without detecting
XX non-related viruses. The primer sets for HIV-1 and HIV-2 are compatible
XX with each other, and can be combined to form a co-amplification assay
XX for HIV-1 and HIV-2. Using more than one primer set to amplify target
XX nucleic acid sequences which overlap a common probe region maximises
XX strain sensitivity and robustness.

SQ Sequence 35 BP; 6 A; 10 C; 5 G; 10 T; 4 other;

Query Match 17.0%; Score 15.8; DB 20; Length 35;
Best Local Similarity 63.0%; Pred. No. 2.4e+04;
Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

67 GTGGGCGCTCCGAGAAACATTGAGTG 93
|||||:|||||
30 GTGSSSCCAAGAGAGATTGAGTG 4

RESULT 29
AAZ28217/C
ID AAZ28217 standard; DNA; 39 BP.
XX
XX AAZ28217;
AC
XX 20-DEC-1999 (first entry)
DT
XX
XX Mouse splice acceptor sequence #4.
DE
XX Gene trapping; splicing; integration; mutation; genome; intron; exon;
KW splice acceptor; identification; ss.
XX
XX Synthetic.
OS Mus musculus.
XX
XX WO950426-A1.
PN
XX 07-OCT-1999.
PD
XX
XX 26-MAR-1999; 99WO-US06474.
PE
XX
XX 27-MAR-1998; 98US-0079729.
PR 08-APR-1998; 98US-0057328.
PR 14-APR-1998; 98US-0081727.
PR
XX
XX (LEXI-) LEXICON GENETICS INC.
PA
XX
XX Zambrowicz B, Friedrich GA, Sands AT;
PI
XX
XX WPI; 1999-591324/50.
DR
XX
XX New gene trapping vectors, useful for identifying, activating or
PT mutating genes in eukaryotic cells
PS
XX
XX Disclosure; Page 13; 74pp; English.

This sequence represents a murine splice acceptor sequence for use in a 5' gene trap cassette. Gene trapping can be used to simultaneously identify and mutate genes. Gene trap vectors are designed to integrate into introns or genes in a manner that allows the cellular splicing machinery to splice vector-encoded exons to cellular mRNAs. A gene trap vector may contain a 5' and/or a 3' gene trap cassette. A 5' gene cassette may comprise a strong splice acceptor sequence, selectable marker sequences and a polyadenylation site, but not a promoter. Similarly a 3' cassette may comprise a promoter region, an exon (typically characterized by a translation initiation codon and open reading frame and/or internal ribosome entry site), a splice donor sequence and optionally intronic sequences. After integration of the vector, transcription and splicing, chimeric RNAs are produced comprising the gene trap cassette spliced to an endogenous exon encoded within the target cell genome. Such gene trapping can be used to identify novel genes and in screening e.g., to identify the genetic basis of diseases (such as cancer) or phenotypes, especially in the analysis of single nucleotide polymorphisms. The vector can also be introduced into a cell to activate expression of a naturally occurring cellular gene, useful to study gene function. They can be used to produce mutated cells or animals, and are useful in screening, for example, to identify mutations associated with tumorigenic phenotypes. They can also be used to create cDNA libraries of cells, useful for large scale genetic analysis of the genome and to identify novel and mutated genes. The vectors are more efficient (e.g., their use identified 13-fold more genes) than conventional 3' gene trap vectors that rely on gene trapping as detected by antibiotic selection.

CC Use of vectors incorporating 5' gene trap cassettes increase the
CC probability of identifying the 5' ends of gene open reading frames,
CC important because these are difficult to obtain by conventional methods,
CC and often code for the signal sequence in secreted and transmembrane
CC proteins, an important group for potential drug targets.

Sequence 39 BP; 7 A; 17 C; 7 G; 8 T; 0 other;

Query Match 17.0%; Score 15.8; DB 20; Length 39;
Best Local Similarity 74.1%; Pred. No. 2.5e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

67 GTGGGCGCTCCGAGAAACATTGAGTG 93
|||||:|||||
33 GCGGCTCTCCGAGGAGACAGTGAGTG 7

RESULT 30
AAA29286/C
ID AAA29286 standard; DNA; 39 BP.
XX
XX AAA29286;
AC
XX 12-SEP-2000 (first entry)
DT
XX
XX Splice acceptor sequence 5 for 5' gene trap cassette.
DE
XX
XX Splice acceptor; vector; gene trap; gene discovery; cloning; analysis;
KW shuttling; gene activation; over-expression; ss.
XX
XX Synthetic.
OS
XX
XX WO20031236-A2.
PN
XX
XX 02-JUN-2000.
PD
XX
XX 19-NOV-1999; 99WO-US27366.
PE
XX
XX 20-NOV-1998; 98US-0109302.
PR 25-MAR-1999; 99US-0276533.
PR
XX
XX (LEXI-) LEXICON GENETICS INC.
PA
XX
XX Zambrowicz B, Friedrich GA, Lillberg S, Sands AT;
PI
XX
XX WPI; 2000-400033/34.
DR
XX
XX Recombinant vectors for use in, for example, gene discovery, gene
PT cloning and gene mutation
PS
XX
XX Disclosure; Page 13; 78pp; English.

AAA29282-92 are examples of suitable splice acceptor sequences for use in construction of genetically incorporated vectors comprising 5' gene trap cassettes. The vectors incorporate structural elements which, after integration into the host cell genome, enhance the number of cellular genes that can be identified and mutated. A 5' gene trap cassette comprises a splice acceptor (SA), an exon sequence (Ex1) located 3' to the SA, which encodes a marker enabling the identification of a cell expressing the exon and a polyadenylation sequence defining the 3' end of Ex1. The vectors may be used for gene discovery, gene cloning, gene mutation, gene regulation, shuttling nucleic acid sequences throughout the genome and gene activation and over expression. The vectors can be used to trap genes with a high level of efficiency regardless of whether the genes are normally expressed in the cell type into which the vector is incorporated. Cells harboring the vectors can be screened using automated gene identification assays such as 3' RACE. Using these vectors, it is possible to produce large numbers of mutations and rapidly identify the mutated or trapped genes.

Sequence 39 BP; 7 A; 17 C; 7 G; 8 T; 0 other;
Query Match 17.0%; Score 15.8; DB 21; Length 39;

XX	Unidentified.	OS
PN	WM0200240130-A1.	PN
PD	23-MAY-2002.	PD
PF	05-SEP-2001, 2001WO-US27495.	PF
PR	16-NOV-2000, 2000US-0714579.	PR
PA	(TRAN-) TRANSGENOMIC INC.	PA
PI	Gjerde DT, Haeefele RM, Hanna CP, Hornby D, Kuklin AI, Taylor PD;	PI
DR	WPI; 2002-566535/60.	DR
PT	Separation of a mixture of single-stranded polynucleotides e.g. DNA, or	PT
PT	RNA, comprises applying the mixture to a polymeric separation medium	PT
XX	having non-polar surfaces, and then separating the mixture	XX
PS	Example 24; Page 53; 91pp; English.	PS
CC	The invention comprises a method of separating a mixture which contains	CC
CC	single-stranded polynucleotides. The method of the invention involves	CC
CC	applying the mixture to a polymeric separation medium having non-polar	CC
CC	surfaces. The non-polar surfaces are free from multivalent cations	CC
CC	(preferably chromium, iron, nickel and/or copper) and are free to bind or	CC
CC	interfere with the polynucleotides. The method of the invention is useful	CC
CC	for separating a mixture that contains single-stranded polynucleotides	CC
CC	(e.g. DNA and RNA) having lengths from 5 - 200 up to 2000 - 20000	CC
CC	nucleotides from impurities (e.g. failure sequences, salts and/or	CC
CC	proteins). The method of the invention allows separation to be achieved	CC
CC	within 10 - 30 minutes, in contrast to conventional gel chromatography	CC
CC	which can require hours or days. The present DNA sequence represents an	CC
XX	oligonucleotide that was used in an example of the invention.	XX
SO	Sequence 44 BP; 11 A; 11 C; 11 G; 11 T; 0 other;	SO
Query Match	17.0%; Score 15.6; DB 24; Length 44;	
Best Local Similarity	65.7%; Pred. No. 2.5e+04;	
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0		
OY	32 CAATGCGCTGGTTCCACACTATCGAATGAGCT 66	
DB		
	35 CAATGCGCTGGTTGGCGACTCTCATCGGAGCTCTACT 1	
RESULT 34		
AAAX26503/C		
ID	AAAX26503 standard; DNA; 46 BP.	
XX		
AC	AAAX26503;	
XX		
DT	28-MAY-1999 (first entry)	
DE	WO 9909191 SeqID #5.	
XX		
OS	Cancer; treatment; vector; recombinase gene; transcription factor;	
XX	selective cell killing; gene therapy; primer; ss.	
XX	Synthetic.	
PM	WO9909191-A1.	
XX		
PD	25-FEB-1999.	
XX		
PF	02-JUL-1998; 98WO-JP02993.	
PR	20-AUG-1997; 97JP-022651.	
PA	(DNAM-) DNAMVEC RES INC.	
PI	Hasegawa M, Takeda K, Yokoi H;	

```

XX MPI: 1999-181048/15.
XX
XX
PT Gene expression specific to cells free from specific transcription
PT Factor with constructed recombinase expression unit after infecting
PT cells - allowing expression of target gene in gene therapy,
PT particularly in cancer treatment
XX
XX
PS Example 1: Page 12; 49pp; Japanese.
XX
XX This invention describes a vector containing a recombinase gene which
XX is controlled by (1) a promoter and action of which is in turn dependent
XX on a specific transcription factor and (2) a desired gene to be expressed
XX and two target sequences of the recombinase. Also described in the
XX invention are (1) a host cell for introduction of the vector and (11) an
XX in vitro technique in which killing of cells without the specific
XX transcription factor is selectively performed after the vector is
XX introduced into a host cell by an in vitro technique. The technique is
XX used for gene therapy e.g. in cancer treatment. The products of the
XX invention allow the use of a specific vector specifically and safely,
XX there is little toxicity.
XX
XX Sequence 46 BP, 12 A; 16 C; 8 G; 10 T; 0 other:
XX
XX
SQ
XX
XX Query Match 17.0%; Score 15.8; DB 20; Length 46;
XX Best Local Similarity 74.1%; Pred. No. 2.6e+04;
XX Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 25 TGGGTGACAAATGCTTGCTTCAACAC 51
XX ||||| ||||||| |||||
XX 40 TGTGACGACGGGCAATGCTTAAACAC 14
XX
XX
RESULT 35
XX ID AAZ67047
XX AAZ67047 standard; DNA: 47 BP.
XX
XX AAZ67047:
XX
XX 10-SEP-2001 (first entry)
XX
XX Human map-related diallelic marker SPO ID NO:1394.
XX
XX Human genome; diallelic marker: high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(24,g)
XX /*tag=a
XX /standard_name="single nucleotide polymorphism"
XX
XX W09954500-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 21-APR-1999; 99WC-1B00822.
XX
XX PR 21-APR-1998; 98US-0082614.
XX PR 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel diallelic markers used to construct a high density disequilibrium
XX map of the human genome -

```


PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shetton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 PI
 DR WPI: 2000-572271/53.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX
 PS Example 7; Page 151; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic
 CC anemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 CC
 SQ Sequence 48 BP; 14 A; 16 C; 8 G; 10 T; 0 other;
 OY Query Match 17.0%; Score 15.8; DB 21; Length 48;
 DB Best Local Similarity 74.1%; Pred. No.2.6e+04;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 62 TGAAGTCGGGCTCCAGAAACATTG 88
 DB 16 TCACTATAGGCGCTCCAGAAACCTCG 42

RESULT 38
 ABR52192
 ID ABR52192 standard; DNA: 27 BP.
 AC ABR52192;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human OGBbeta14 cDNA specific real time PCR probe.
 XX
 KW OGBbeta14; human; ss; antifertility; contraceptive; antithyroid;
 KW chromosome 14; steroidogenesis; reproductive disease; fertility;
 KW contraception; pregnancy; menopause; dysmenorrhea; thyroid malfunction;
 KW thyroid deficiency; muscle atrophy; homeostasis; probe; TagMan.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "6-FAM labelled"
 FT modified_base 27
 FT /*tag= b
 FT /note= "3' TAMRA labelled"
 XX
 PN W0200230978-A1.
 XX
 PD 18-APR-2002.
 XX
 PE 06-OCT-2000; 2000WO-US27797.
 XX
 PF 06-OCT-2000; 2000WO-US27797.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Murphy AJ;
 PI
 DR WPI: 2002-435439/46.
 XX
 PT Novel isolated human OGBbeta14 polypeptide, useful in the treatment and
 PT diagnosis of reproductive diseases such as fertility, contraception,
 PT thyroid malfunction, altered cellular metabolism and bone homeostasis
 XX
 PS Example 3; Page 31; 51pp; English.
 XX
 CC This invention relates to the nucleotide and protein sequences of a
 CC novel isolated human OGBbeta14 protein. The gene encoding this protein is
 CC located on human chromosome 14. This protein may act as a cell function
 CC regulator, as an stimulator of steroidogenesis or to inhibit the binding
 CC of intact human chorionic gonadotropin (hCG) to its receptor. The
 CC nucleotide sequence of the invention is useful to identify and obtain a
 CC full length human OGBbeta14 cDNA sequence and oligomers of this sequence
 CC is useful to identify a disorder or disease with altered human OGBbeta14
 CC expression and provide a method for monitoring progress of a patient
 CC during drug therapy. An antibody against the human OGBbeta14 is useful
 CC in assays to identify a disorder or disease with altered human OGBbeta14
 CC expression and monitor the progress of a patient during drug therapy.
 CC which altered human OGBbeta14 expression is implicated. The protein is
 CC useful in assays to evaluate the role of a specific human OGBbeta14
 CC in normal, diseased or therapeutically treated cells. The nucleotide
 CC sequence of the invention is useful for treating diseases or disorders
 CC including reproductive diseases such as fertility, contraception,
 CC maintenance of pregnancy, menopause, dysmenorrhea, diseases related to
 CC thyroid malfunction such as thyroid deficiency or hyperactive thyroid
 CC leading to altered cellular metabolism, muscle atrophy, growth,
 CC development, blood and bone homeostasis. The present sequence represents
 CC the human OGBbeta14 cDNA specific real time Tagman probe used
 CC to quantitate expression of the human OGBbeta14 sequence of the
 CC invention.
 XX
 SQ Sequence 27 BP; 9 A; 7 C; 7 G; 4 T; 0 other;

Query Match 16.8%; Score 15.6; DB 24; Length 27;
 Best Local Similarity 81.8%; Pred. No. 2.6e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCTGGAGCACTCCATTCGT 22
 || ||||| || |||||
 DB 2 GAGCTGGAGCAACCATTCGT 23

RESULT 39
 AAH21862
 ID AAH21862 standard; DNA; 30 BP.
 AC AAH21862;
 XX
 XX 16-AUG-2001 (first entry)
 DE Mouse N-calcium channel alpha 1B subunit PCR primer SEQ ID NO:5.
 XX
 KW Mouse; N-calcium channel alpha 1B subunit; blood pressure control;
 KW N-calcium channel knockout animal; blood glucose level control;
 KW pain transfer; hypotensive; analgesic; PCR primer; ss.
 OS Mus musculus.
 XX
 PN WO200130137-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-JP07503.
 XX
 PR 26-OCT-1999; 99JP-0303809.
 PR 16-FEB-2000; 2000JP-0037839.
 PR 31-AUG-2000; 2000JP-0261979.
 XX
 PA (EISA) EISAI CO LTD.
 XX
 PI Iino M, Miyamoto N, Takahashi E, Oki T, Yoshinaga T, Hatakeyama S;
 PI Nildome T, Sawada K, Nishizawa Y, Tanaka I;
 XX
 DR WPI; 2001-300406/31.
 XX
 XX N-type calcium channel deficient non-human animals useful for screening
 PT for new drugs -
 XX
 PS Example 1; Page 57; 64pp; Japanese.
 CC The present invention describes an N-type calcium channel deficient
 CC non-human animal whose gene for the calcium channel has been disrupted.
 CC The gene that is disrupted encodes the N-type calcium channel alpha 1B
 CC subunit. Also described are: (1) a method for assaying usefulness of
 CC substances using the animal; (2) a method for screening for substances
 CC with potential pharmacological use; (3) useful substances found by the
 CC method; and (4) a method for producing pharmaceuticals using this method
 CC (specifically methods for producing a hypotensive drug, a pain killer
 CC and a drug for lowering blood sugar and the substances themselves). The
 CC N-type calcium channel deficient non-human animal can be used for
 CC screening substances for pharmaceutical use. Active substances include
 CC a hypotensive drug, a pain killer and a drug for lowering blood sugar.
 CC The present sequence represents a PCR primer used in the isolation of
 CC the mouse N-calcium channel alpha 1B subunit, which is used in an
 CC example from the present invention.
 XX
 SO Sequence 30 BP; 4 A; 8 C; 11 G; 7 T; 0 other;

Query Match 16.8%; Score 15.6; DB 22; Length 30;
 Best Local Similarity 81.8%; Pred. No. 2.7e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 71 GGCTCCAGAAACATTGAGGT 92
 ||||| || |||||
 DB 1 GGCTCCAGGTGACAGTGGT 22

RESULT 40
 AAI30206/c
 ID AAI30206 standard; DNA; 31 BP.
 XX
 AC AAI30206;
 XX
 XX 18-OCT-2001 (first entry)
 DE Human single nucleotide polymorphism (SNP) SPTBN1 7.
 XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(16,T)
 FT /*tag= a
 /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200166800-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US07268.
 XX
 PR 07-MAR-2000; 2000US-0187510.
 PR 22-MAY-2000; 2000US-0206129.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-522952/57.
 XX
 XX Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or
 PT severity of a particular phenotype or disorder (e.g. diabetes)
 PT associated with a particular genotype -
 XX
 PS Claim 1; Page 72; 145pp; English.
 CC The invention relates to the identification of nucleic acid molecules
 CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.
 XX
 SO Sequence 31 BP; 7 A; 6 C; 13 G; 5 T; 0 other;

Query Match 16.8%; Score 15.6; DB 22; Length 31;
 Best Local Similarity 81.8%; Pred. No. 2.7e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 15 CCATTGCTGGGACAAATG 36
 || ||||| || |||||
 DB 22 CCCTCTGCTGATGCCAATG 1

RESULT 41
 ABL41371/c
 ID ABL41371 standard; DNA; 33 BP.
 XX
 AC ABL41371;
 XX
 XX 29-MAY-2002 (first entry)
 DE
 XX

DE Human transcription aporepressor CTCF 10.23 PCR primer SEQ ID NO 6.
 XX
 XX
 KW Human: transcription aporepressor; CCCG-conjugated factor; CTCF;
 KW gene therapy; tumour; development; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1326974-A.
 XX
 PD 19-DEC-2001.
 XX
 PF 07-JUN-2000; 2000CN-0116361.
 XX
 PR 07-JUN-2000; 2000CN-0116361.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI, 2002-217567/28.
 XX
 PT New polypeptide-human transcription arrestin CCCG-conjugated factor
 PT (CTCF)10.23 and polynucleotide for encoding such polypeptide -
 XX
 PS Example 4; Page 19 (Disclosure); 34pp; Chinese.
 XX
 CC The invention relates to human transcription aporepressor
 CC CCCG-conjugated factor (CTCF) 10.23, the polynucleotide encoding this
 CC polypeptide and DNA recombinant processes to produce the polypeptide. The
 CC present invention also discloses the application of the polynucleotide
 CC for gene therapy. The present invention discloses the antagonist for
 CC resisting the polypeptide and its treatment effect. The present invention
 CC also discloses the method of applying the polypeptide in treating various
 CC diseases, such as common tumours, development disturbance disease. The
 CC present sequence is that of a PCR primer, useful in examples of the
 CC invention.
 XX
 SQ Sequence 33 BP; 11 A; 8 C; 6 G; 8 T; 0 other;
 XX
 QY Query Match 16.8%; Score 15.6; DB 24; Length 33;
 Best Local Similarity 81.8%; Pred. No. 2.8e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 57 GAATGACTGTCGGGCTCCA 78
 |||||
 24 GAATGACTGTTGAGATCCA 3
 RESULT 42
 AAZ07103
 ID AAZ07103 standard; DNA; 35 BP.
 XX
 AC AAZ07103;
 XX
 DE 07-OCT-1999 (first entry)
 XX
 DE Recombinant PC gene PYC1 PCR primer b-4.
 XX
 KW PYC1; PYC1; PC gene; organic acid; pyruvic acid carboxylase;
 KW aerobic coryneform bacterium; Brevibacterium Flavum MJ-233;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Saccharomyces cerevisiae.
 XX
 PN JP11196888-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 16-JAN-1998; 98JP-0020361.
 XX
 PR 16-JAN-1998; 98JP-0020361.
 XX

PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI, 1999-471888/40.
 XX
 PT Preparing organic acids with a microorganism having a recombinant
 PT pyruvic acid carboxylase gene - using reaction solution containing
 PT carbonate ion or hydrogen-carbonate ion
 XX
 PS Example 5; Page 10; 12pp; Japanese.
 XX
 CC The present invention describes the preparation of organic acids with
 CC the anaerobic action of an aerobic coryneform bacterium having a
 CC recombinant pyruvic acid carboxylase (PC) gene, where the PC gene can be
 CC derived from microorganisms, animals or plants, especially human, mouse,
 CC rat, yeast, or microorganisms of Corynebacterium, Bacillus, Rhizobium or
 CC Escherichia spp., or its extract with organic materials in a reaction
 CC solution containing carbonate ion or hydrogen-carbonate ion, or CO₂.
 CC Particularly prepared by addition of carbonic acid or hydrogen-carbonic
 CC acid or their salts, or CO₂. The aerobic coryneform bacterium of
 CC Brevibacterium flavum, is preferably Brevibacterium flavum MJ-233
 CC (FERM BP-1497). The method gives a high yield of organic acids
 CC (e.g. succinic acid) with an aerobic coryneform bacterium,
 CC Brevibacterium flavum MJ-233, having a recombinant PC gene (e.g. PYC1
 CC and PYC2). The present sequence represents a PCR primer for a recombinant
 CC PC gene, designated PYC1, used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 35 BP; 8 A; 9 C; 7 G; 11 T; 0 other;
 XX
 QY Query Match 16.8%; Score 15.6; DB 20; Length 35;
 Best Local Similarity 81.8%; Pred. No. 2.8e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 34 ATGCTTGCTTCAACATATC 55
 |||||
 14 ATGCTTGCTTCAACAGGAC 35
 RESULT 43
 AA99100
 ID AA99100 standard; DNA; 43 BP.
 XX
 AC AA99100;
 XX
 DE 09-MAR-1999 (first entry)
 XX
 DE DNA methyltransferase genomic fragment.
 XX
 KW DNA methyltransferase; DNA Methylase; antisense oligonucleotide; human;
 KW cellular growth; tumour growth inhibition; silenced gene activation;
 KW beta thalassemia; sickle cell anemia; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9854313-A2.
 XX
 PD 03-DEC-1998.
 XX
 PF 29-MAY-1998; 98WO-1B01107.
 XX
 PR 17-DEC-1997; 97US-0069865.
 XX
 PR 30-MAY-1997; 97US-0866340.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Bigey P, Ramchandani S, Szyf M;
 XX
 DR WPI, 1999-059833/05.
 XX
 PF New DNA methyltransferase nucleotide sequences - used particularly
 PF to develop antisense oligonucleotides for diagnostic and therapeutic
 PF purposes, particularly for inhibiting tumour growth
 XX

PS Claim 1: Page 44; 108pp; English.

XX
CC AAV99091-128 represent DNA methyltransferase (DNA Methylase) genomic
CC fragments. The sequences together sequentially produce the full
CC length sequence AAV99128. The sequences can be used to derive antisense
CC oligonucleotides which inhibit DNA Methylase expression. The antisense
CC oligonucleotides can be used in investigating the role of DNA Methylase
CC in cellular growth. They can be administered at different points in
CC the cell cycle, or in conjunction with promoters or inhibitors of cell
CC growth to determine the role of DNA Methylase in the growth of the cell
CC type of interest. The antisense oligonucleotides can also be used for
CC inhibiting tumour growth in a mammal, or to activate silenced genes to
CC provide a missing gene function. This ameliorates disease symptoms,
CC e.g. in beta thalassemia and sickle cell anemia. The antisense
CC oligonucleotides can also be used as an analytical and diagnostic tools
CC and a potentiators of transgenic plant and animal studies.

SQ Sequence 43 BP; 2 A; 6 C; 13 G; 22 T; 0 other;

Query Match 16.8%; Score 15.6; DB 20; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+04;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 18 TTCGCGTGGTGAACATGCGTTGTTCA 47
||||| ||||| ||||| ||||| |||||
Db 8 TTCTGTTGGGTGGTGGTCTTGTGTTGCA 37

RESULT 44

AAZ68364
ID AAZ68364 standard; DNA; 47 BP.

XX AAZ68364;

DT 10-SEP-2001 (first entry)

DE Human map-related diallelic marker SEQ ID NO:2711.

XX Human genome; diallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

OS diagnosis; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

OS

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Location/Qualifiers
replace(24,T)
/*tag= a

/standard_name= "single nucleotide polymorphism"

PN

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PA

XX

XX

XX

XX

XX

XX

XX

(GEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

XX

XX

XX

XX

XX

XX

WPI; 2000-013267/01.

XX

XX

XX

XX

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XX

XX

21-APR-1999; 99WO-1B00822.

XX

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XX

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XX

XX

21-APR-1998; 98US-0082614.

XX

XX

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23-NOV-1998; 98US-0109732.

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Claim 3: Page 808; 2745pp; English.

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AAZ65654 to AAZ69578 represent human diallelic markers from the present

XX

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invention, which contain a polymorphic base at position 24 of their

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XX

XX

nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

XX

XX

XX

XX

XX

XX

XX

CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the sequence listing
CC from the present invention.

SQ Sequence 47 BP; 16 A; 12 C; 4 G; 15 T; 0 other;

Query Match 16.8%; Score 15.6; DB 21; Length 47;
Best Local Similarity 70.0%; Pred. No. 3.1e+04;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 37 CCTGGTTTCAACATATCGAATGCACT 66
||||| ||||| ||||| ||||| |||||
Db 15 CCTGCTTTTCAAAACATATCGAATGCAAT 44

RESULT 45

AAI73671
ID AAI73671 standard; DNA; 50 BP.

XX AAI73671;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:612.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX WO200140521-A2.

XX

XX

XX

XX

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XX

XX

XX

XX

XX

XX

Claim 1: Page 241; 2653pp; English.

AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide

XX sequences (I), which contain single nucleotide polymorphisms (SNPs).

XX AAI73114 to AAI73329 represent peptides related to human polymorphic

XX polynucleotide sequences. The sequences can be used in gene and protein

XX therapy, and in vaccine production. (I) and the polypeptides encoded by

XX associated with inappropriate expression of polymorphic polypeptides.

XX For example, (I) may be used to treat disorders by rectifying mutations

XX or deletions in a patient's genome that affect the activity of

XX polypeptides by expressing inactive proteins or to supplement the

XX patients own production of polypeptide. Additionally, (I) and its

XX complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (1) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX

SQ Sequence 50 BP; 8 A; 16 C; 17 G; 9 T; 0 other;

Query Match 16.8%; Score 15.6; DB 22; Length 50;

Best Local Similarity 70.0%; Pred. No. 3.2e+04;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 16 CATTGCTGCTGGGTGACATGCTTGT 45
DB 12 CTTGCTGCTGGGTGACATGCTTGT 41

RESULT 46

AAH48692/C
ID AAH48692 standard; DNA; 50 BP.

XX AAH48692;

DT 19-OCT-2001 (first entry)

XX Human G-protein subunit Gbeta3 intron 9 DNA fragment #5.

XX Human; G-protein subunit Gbeta3; variant; high blood pressure; asthma;

KW hypertension; cardiac infarction; coronary disease; heart disease;

KW circulatory disease; diabetes; psychiatric disease; Crohn's disease;

KW immunological disease; psoriasis; colitis ulcerosa;

transplant rejection; ds.

XX Homo sapiens.

OS DE10030945-A1.

XX 09-AUG-2001.

XX 24-JUN-2000; 2000DE-1030945.

XX 03-FEB-2000; 2000DE-1004681.

XX 21-FEB-2000; 2000DE-1007587.

XX (SIFP/) SIFFERT W.

XX Siffert W;

XX WPI; 2001-490007/54.

XX Disclosure; Page 3; 14pp; German.

CC This invention describes a novel use for sequence variants of the human
CC G-protein beta3 subunit to predict physiological and pathological
CC pathways in the human body. The invention may be used to detect, detect
CC predisposition for, give a prognosis of, or treat a variety of diseases
CC including high blood pressure, hypertension, cardiac infarction, coronary
CC disease and other heart or circulatory diseases, diabetes, psychiatric
CC diseases, immunological diseases, asthma, psoriasis, Crohn's disease,
CC colitis ulcerosa, transplant rejection, HIV or Hepatitis B or C. This
CC sequence represents a fragment of the human G-protein Gbeta3 subunit
CC intron 9 which is used to illustrate the method of the invention.

SQ Sequence 50 BP; 14 A; 13 C; 19 G; 4 T; 0 other;

Query Match 16.8%; Score 15.6; DB 22; Length 50;

Best Local Similarity 70.0%; Pred. No. 3.2e+04;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 16 CATTGCTGCTGGGTGACATGCTTGT 45
DB 40 CAGCTCCCTGCTGCTGCTTGTGTT 11

RESULT 47

AAH48693/C
ID AAH48693 standard; DNA; 50 BP.

XX AAH48693;

DT 19-OCT-2001 (first entry)

XX Human G-protein subunit Gbeta3 intron 9 DNA fragment #6.

XX Human; G-protein subunit Gbeta3; variant; high blood pressure; asthma;

KW hypertension; cardiac infarction; coronary disease; heart disease;

KW circulatory disease; diabetes; psychiatric disease; Crohn's disease;

KW immunological disease; psoriasis; colitis ulcerosa;

transplant rejection; ds.

XX Homo sapiens.

OS DE10030945-A1.

XX 09-AUG-2001.

XX 24-JUN-2000; 2000DE-1030945.

XX 03-FEB-2000; 2000DE-1004681.

XX 21-FEB-2000; 2000DE-1007587.

XX (SIFP/) SIFFERT W.

XX Siffert W;

XX WPI; 2001-490007/54.

XX Disclosure; Page 3; 14pp; German.

CC This invention describes a novel use for sequence variants of the human
CC G-protein beta3 subunit to predict physiological and pathological
CC pathways in the human body. The invention may be used to detect, detect
CC predisposition for, give a prognosis of, or treat a variety of diseases
CC including high blood pressure, hypertension, cardiac infarction, coronary
CC disease and other heart or circulatory diseases, diabetes, psychiatric
CC diseases, immunological diseases, asthma, psoriasis, Crohn's disease,
CC colitis ulcerosa, transplant rejection, HIV or Hepatitis B or C. This
CC sequence represents a fragment of the human G-protein Gbeta3 subunit
CC intron 9 which is used to illustrate the method of the invention.

SQ Sequence 50 BP; 15 A; 13 C; 18 G; 4 T; 0 other;

Query Match 16.8%; Score 15.6; DB 22; Length 50;

Best Local Similarity 70.0%; Pred. No. 3.2e+04;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 16 CATTGCTGCTGGGTGACATGCTTGT 45
DB 40 CAGCTCCCTGCTGCTGCTTGTGTT 11

RESULT 48

ABL50681/C
ID ABL50681 standard; DNA; 28 BP.

XX ABL50681;

XX 19-JUN-2002 (first entry)
 DT XX

DE Rat G protein-coupled receptor protein PCR primer SEQ ID NO:30.
 XX

KW Rat; r2a01; r2a02; G protein-coupled receptor; GPCR; antidiarrheic;
 XX laxative; drug development; digestive organ disease; colitis; diarrhoea;
 KM constipation; malabsorption syndrome; diagnosis; gene therapy;
 KM PCR primer; ss.

OS Rattus sp.
 XX

PN M0200216607-A1.
 XX

PD 28-FEB-2002.
 XX

PF 23-AUG-2001; 2001MO-JP07209.
 XX

PR 24-AUG-2000; 2000JP-0253862.
 XX

PA (TAKE) TAKEDA CHEM IND LTD.
 XX

PI Terao Y, Shintani Y;
 XX

DR WPI; 2002-269361/31.
 XX

PT Human and rat brain-originated G protein-coupled receptor proteins and
 PT encoded DNAs, for developing drugs to treat diseases of the digestive
 PT organs, e.g. colitis, diarrhoea, constipation and mal-absorption
 PT syndrome -
 XX

PS Example 4; Page 71; 135pp; Japanese.
 XX

CC The present invention describes human and rat brain-originated
 CC G protein-coupled receptor (GPCR) proteins. The GPCR sequences have
 CC antidiarrheic and laxative activities. The GPCR sequences can be used
 CC for developing drugs to treat diseases of the digestive organs,
 CC e.g. colitis, diarrhoea, constipation and malabsorption syndrome,
 CC including gene diagnosis and therapy. The present sequence represents
 CC a PCR primer for rat GPCR, which is used in an example from the present
 CC invention.
 XX

SQ Sequence 28 BP; 7 A; 11 C; 8 G; 2 T; 0 other;

Query Match 16.6%; Score 15.4; DB 24; Length 28;
 Best Local Similarity 76.0%; Pred. No. 3.1e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 51 CTATCGAATGTCGTCGGGCT 75
 ||||| ||||| ||||| |||||

DB 26 CTATCGAATGTCGTCGGGCT 2

RESULT 49

AAZ8883/C
 ID AAZ8883 standard; DNA; 30 BP.

AC AAZ8883;
 XX

DT 26-MAY-2000 (first entry)
 XX

DE Human wolframin intron 1/exon 2 boundary DNA fragment.
 XX

KW Wolframin; human; transmembrane protein; diagnosis; therapy;
 KM Wolfram Syndrome; psychiatric disease; gene therapy; ss.

OS Homo sapiens.
 XX

PN DE19845277-C1.
 XX

PD 09-MAR-2000.
 XX

PF 01-OCT-1998; 98DE-1045277.
 XX

XX 01-OCT-1998; 98DE-1045277.
 PR (UWM-) UNIV MÜNCHEN MAXIMILIANS LUDWIG.
 PA
 XX

PI Strom T, Weitinger T;
 XX

DR WPI; 2000-184136/17.
 XX

PT Wolframin, a transmembrane protein and related DNA useful for diagnosis
 PT and therapy of Wolfram Syndrome, especially where there is a tendency
 PT to psychiatric disease -
 XX

PS Disclosure; Page 8; 26pp; German.
 XX

CC This invention describes a novel human transmembrane protein, wolframin.
 CC Wolframin and DNA encoding it are useful for diagnosis and/or therapy of
 CC Wolfram Syndrome, in particular where there is a tendency to psychiatric
 CC disease. The products of the invention can be used for gene therapy.
 CC This sequence represents the intron 1/exon 2 boundary of human
 CC wolframin genomic DNA.
 XX

SQ Sequence 30 BP; 5 A; 8 C; 7 G; 10 T; 0 other;

Query Match 16.6%; Score 15.4; DB 21; Length 30;
 Best Local Similarity 76.0%; Pred. No. 3.2e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 10 GCACCTCATCTCGCTGACAA 34
 ||||| ||||| ||||| |||||

DB 30 GCACCTCATCTCGCTGACAA 6

RESULT 50

AAT04205
 ID AAT04205 standard; DNA; 31 BP.

AC AAT04205;
 XX

DT 25-JAN-1996 (first entry)
 XX

DE PCR primer oligo B for mitochondrial targeting sequence of the
 DE matrix processing peptidase.
 XX

KW Mitochondrial targeting sequence; matrix processing peptidase;
 KM PCR primer; ss.

OS Synthetic.
 XX

PN M09524487-A.
 XX

PD 14-SEP-1995.
 XX

PF 07-MAR-1995; 95WO-EP00859.
 XX

PR 19-OCT-1994; 94DE-4438821.
 XX

PR 09-MAR-1994; 94DE-4408629.
 XX

PR 22-SEP-1994; 94DE-4435366.
 XX

PA (AGRE) HOECHST-SCHERING AGREVO GMBH.
 XX

PI la Cognata U, Landschutze V, Müller-rober B, Landschuetze V;
 XX

PI Müller-rober B;
 XX

DR WPI; 1995-328278/42.
 XX

PT DNA encoding plant citrate synthase - used to regulate flower formation,
 PT to improve storage of tubers, etc. and to reduce sprouting
 XX

PS Example; Page 46; 87pp; English.
 XX

CC A DNA sequence which codes for the mitochondrial targeting sequence
 CC of the matrix processing peptidase (MPP) was isolated by PCR from a

CC plusescript plasmid which contained the cDNA sequence of the MPP
 CC using the oligos AAT04204 and AAT04205. The resulting DNA fragment
 CC comprised the nts 299-397 of the sequence in Braun et al. 1992,
 CC EMB0 J. 11:3219-3227, which codes for the MPP. An Asp 718 cleavage
 CC site was inserted at the 5' end of the sequence by oligo a. Oligo b
 CC inserted a BamHI site at the 3' end of the sequence.

XX
 SO Sequence 31 BP; 7 A; 8 C; 9 G; 7 T; 0 other;

Query Match 16.6%; Score 15.4; DB 16; Length 31;
 Best Local Similarity 76.0%; Pred. No. 3.2e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 34 ATGCCTTGTTCAACACTATCGGA 58
 ||||||| ||||| |||||
 Db 7 ATCCCTTGTTGCAACAGCAGCTGA 31

RESULT 51

AAV11384 standard; DNA; 31 BP.

XX AAV11384;

XX 21-JUL-1998 (first entry)

DE Potato matrix processing peptidase PCR primer mlt0-TP2.

XX Acetyl Coenzyme A hydrolase; Acetyl-CoA; ACCoA; transgenic plant;

KW regulate; control; intracellular distribution; metabolite; acetate;

KW isoprenoid; steroid; flavonoid; hormone; fat content; PCR primer; ss.

XX Synthetic.

XX Solanum tuberosum.

XX W09806831-A1.

XX 19-FEB-1998.

XX 07-AUG-1997; 97WO-EP04311.

XX 19-AUG-1996; 96DE-4033374.

XX 08-AUG-1996; 96DE-4032121.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Baeuerlein M, La COGNATA U, Mueller-Roeber B, Willmitzer L;

XX WPI; 1998-159524/14.

XX Example 1; Page 27; 65pp; German.

XX AAV11379-VI1390 are primers used in a method to construct a transgenic

XX plant cell with altered acetyl-coenzyme A (ACCoA) hydrolase metabolism

XX which has higher activity than wild-type cells. Controlling ACCoA

XX hydrolase activity is used to regulate intracellular distribution of

XX metabolites, specifically it increases concentration of acetate, leading

XX to altered production of isoprenoids, steroids, flavonoids, hormones,

XX fats, oils, rubber, alkaloids, sugars and starch and anti-pathogenic

XX agents. A specific application is increasing the fat content (by at

XX least 7%) of oilseed crops, e.g. (especially) rape, soya, sunflower and

XX oil palms, but the method can also be applied to cereals, vegetables,

XX sugar beet, tobacco, cotton or ornamental plants.

XX Sequence 31 BP; 7 A; 8 C; 9 G; 7 T; 0 other;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 34 ATGCCTTGTTCAACACTATCGGA 58
 ||||||| ||||| |||||
 Db 7 ATCCCTTGTTGCAACAGCAGCTGA 31

RESULT 52

AAV10420 standard; DNA; 31 BP.

XX AAV10420;

XX 02-JUL-1998 (first entry)

DE Potato MPP PCR primer Mito-TP2.

XX Acetyl-CoA-hydrolase; transgenic plant; phenotype trait; potato;

KW altered metabolism; matrix processing peptidase; MPP; PCR primer; ss.

XX Solanum tuberosum.

XX Synthetic.

XX DE19632121-A1.

XX 12-FEB-1998.

XX 08-AUG-1996; 96DE-1032121.

XX 08-AUG-1996; 96DE-1032121.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Baeuerlein M, La Cognata U, Mueller-Roeber B, Willmitzer L;

XX WPI; 1998-121465/12.

XX Example 1; Page 10; 26pp; German.

XX PCR primers AAV10419 & AAV10420 are used to amplify the potato matrix

XX processing peptide (MPP) which is used in a method resulting in the

XX production of transgenic plant cells with altered acetyl-CoA metabolism.

XX The acetyl-CoA hydrolase activity of the cells is greater than that of

XX wild-type cells as a result of the expression of a foreign DNA sequence

XX encoding a protein with acetyl-CoA hydrolase activity. The transgenic

XX plants may have one or more phenotypic traits selected from reduced or

XX increased fatty acid levels in leaves or seeds, increased soluble sugar

XX levels in leaves, increased starch levels in leaves, reduced growth,

XX multiple shoot formation, and change in leaf colour.

XX Sequence 31 BP; 7 A; 8 C; 9 G; 7 T; 0 other;

XX Query Match 16.6%; Score 15.4; DB 19; Length 31;

XX Best Local Similarity 76.0%; Pred. No. 3.2e+04;

XX Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

XX OY 34 ATGCCTTGTTCAACACTATCGGA 58
 ||||||| ||||| |||||
 Db 7 ATCCCTTGTTGCAACAGCAGCTGA 31

RESULT 53

AAF89684 standard; DNA; 39 BP.

XX AAF89684;

XX 23-JUL-2001 (first entry)

DE Probe used to identify FlsY sequences in microorganisms.

XX	FW	FtstY: microorganism identification; bacterial sepsis; septic shock;
XX	KW	bacterial infection; food-borne bacteria; probe; ss.
XX	OS	Streptococcus pneumoniae.
XX	PN	MO200136683-A2.
XX	PD	25-MAY-2001.
XX	PF	16-NOV-2000; 2000MO-US31579.
XX	PR	16-NOV-1998; 98US-0165881.
XX	PR	06-JUN-2000; 2000US-0479457.
XX	PA	(APPO-) APPOLO BIOTECHNOLOGY INC.
XX	PI	Liu Z;
XX	DR	WPI: 2001-355645/37.
XX	PT	Identifying an organism from a population of organisms in a
XX	PT	sample, comprises amplifying a less conserved target sequence present
XX	PT	between a pair of conserved regions -
XX	PS	Claim 33; Page 70; 73pp; English.
XX	CC	The present probe was used to identify FtstY gene sequences from
XX	CC	microorganisms. The probe is used in the method of the invention. The
XX	CC	specification describes a method for identifying an organism among a
XX	CC	population of organisms in a biological sample. The method involves
XX	CC	amplifying a less conserved target sequence present between a pair of
XX	CC	conserved regions, using primers corresponding to a pair of conserved
XX	CC	regions in a genome of a population of organisms, and then using a probe
XX	CC	to detect the amplicon. The method is used for identifying an organism
XX	CC	e.g. a prokaryotic organism, bacteria, virus, or a single cell eukaryotic
XX	CC	organism, among a population of organisms in a biological sample such
XX	CC	as blood, urine, cerebrospinal fluid, sputum, tracheal aspirate or
XX	CC	pleural fluid or in a tissue sample. The method is also useful for
XX	CC	diagnosing a disease or disorder associated with an organism, and for
XX	CC	distinguishing the presence of bacteria and unicellular eukaryotes, or
XX	CC	bacteria and viruses, or bacteria, yeast, paramoeba, trypanosoma,
XX	CC	unicellular eukaryotes or viruses. The method is useful for diagnosing
XX	CC	bacterial sepsis and related septic shock associated with several
XX	CC	bacterial infections, and for testing food-borne bacteria such as
XX	CC	Escherichia coli and Salmonella.
XX	SO	Sequence 39 BP; 6 A; 9 C; 10 G; 14 T; 0 other;
XX	QY	Query Match 16.6%; Score 15.4; DB 22; Length 39;
XX	QY	Best Local Similarity 66.7%; Pred. No. 3.5e+04;
XX	QY	Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX	QY	37 CCTGTGTTCAACACTATGCGAATGTGACTGTC 69
XX	QY	----- ----- -----
XX	QY	7 CCTTGGTGCATATTCACGAAATTCCTCTGTC 39
XX	RESULT 54	
XX	AAT65388	
XX	AAT65388	standard; RNA; 41 BP.
XX	AAT65388;	
XX	DT	
XX	DT	09-SEP-1997 (first entry)
XX	DE	
XX	DE	Human keratinocyte growth factor binding ligand 115.
XX	KW	Human; keratinocyte; growth factor; hKGF; binding ligand;
XX	KW	identification; SLEX; anti-mitogenic; inhibition; cell;
XX	KW	Systematic Evolution of Ligands by Exponential enrichment;
XX	KW	epithelial; proliferation; diagnosis; treatment; cancer;
XX	KW	psoriasis; inflammatory bowel syndrome; ss.

XX	Synthetic.
OS	
XX	
FH	Key
FT	misc_feature
FT	1..41
FT	/+tag=^a
FT	/note= "all pyrimidines are 2'-fluoro modified"
PN	
XX	
PD	
XX	
XX	
PF	
PE	
30-MAY-1996;	96MO-US08014.
XX	
PR	
20-MAR-1996;	96US-0616693.
XX	
PR	
02-JUN-1995;	95US-0458423.
PR	
02-JUN-1995;	95US-0458424.
PR	
05-JUN-1995;	95US-0465591.
PR	
05-JUN-1995;	95US-0465594.
PR	
07-JUN-1995;	95US-0479725.
PR	
07-JUN-1995;	95US-0479783.
XX	
PA	(NEXS-) NEXSTAR PHARM INC.
XX	
PI	
Gold L,	Janjic N, Pagratis N, Ringquist S, Toothman PJ;
XX	
WP1; 1997-034387/03.	
DR	
XX	
PT	
Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF -	
XX	
using SILEX, used in the diagnosis and treatment of proliferative disorders	
XX	
PS	
Claim 61; Page 173; 209pp; English.	
XX	
CC	
The present sequence, a human keratinocyte growth factor (hKGF)	
XX	
binding ligand, was identified by systematic evolution of ligands by exponential enrichment (SELEX). Briefly a candidate mixture of nucleic acids was contacted with hKGF, and nucleic acids having an increased affinity to hKGF partitioned from the remainder of the mixture. The partitioned nucleic acids were then amplified to yield a mixture of nucleic acids enriched for sequences with higher affinity and specificity for binding to hKGF. The ligand is anti-mitogenic and may be used to inhibit epithelial cell proliferation, or in the diagnosis and treatment of hKGF mediated pathological conditions, e.g. psoriasis, cancer and inflammatory bowel syndrome.	
CC	
CC	
CC	
CC	
CC	
CC	
CC	
Sequence 41 BP; 8 A; 10 C; 10 G; 13 U; 0 other;	
XX	
SQL	
Query Match	16.68; Score 15.4; DB 10; Length 41;
Best Local Similarity	52.08; Pred. No. 3.5e+04;
Matches 13; Conservative	6; Mismatches 6; Indels 0; Gaps 0;
OY	
30 GACAAATGCTTGTTTCACACTAT 54	
: : :	
DB	
4 GACGAUGCGGUGGUCUCAUUCUAU 28	
XX	
RESULT 55	
AAVS1124	
ID	AAVS1124 standard; DNA; 41 BP.
XX	
AAVS1124;	
XX	
11-JAN-1999 (first entry)	
DE	
Maize polymorphic marker SZ7G3/G6-1B DNA.	
XX	
Polyomorphic marker; allele-specific; primer: probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back cross; hybrid ancestry; maize; ss.	
KM	
XZea mays.	
OS	

```

XX Key Location/Qualifiers
FH variation 21
FT /*tag= "a"
FT /replace= "g"
FT /note= "polymorphism"
XX
XX WO9824796-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US21782.
XX
XX 07-MAR-1997; 97US-0813507.
XX
XX 02-DEC-1996; 96US-0032069.
XX
XX (AFY-) AFFYMETRIX INC.
XX
XX Landry BS, Lemieux B, Muriigneux A, Sapolsky RJ;
XX
XX WPI; 1998-333252/29.
XX
XX Brassica species allele-specific oligonucleotide probes and primers
XX - useful for plant breeding
XX
XX Claim 1; Page 46; 65pp; English.
XX
XX This DNA sequence is a region of a Zea mays genome which contains a
XX polymorphic marker. This sequence can be used in the construction of
XX allele-specific primers and probes for amplification or hybridisation,
XX e.g. to determine common or disparate ancestry between 2 or more plants,
XX to monitor the genetic contribution of an ancestral plant, to trace the
XX progeny of proprietary plants, in certification of a hybrid plant or to
XX identify the progeny of a back-crossed plant with an ancestral plant.
XX
XX Sequence 41 BP; 7 A; 7 C; 14 G; 13 T; 0 other;
XX
XX Query Match 16.6%; Score 15.4; DB 19; Length 41;
XX Best Local Similarity 66.7%; Pred. No. 3.5e+04;
XX Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX 60 TGTGACTGTGGGCGCTCCAGAAACATTGAGCT 92
XX | | | | | | | | | | | | | | | | | |
XX 8 TGTGACTGTGGGCGCTCCAGACGCTTTTACGT 40
XX
XX RESULT 56
XX AAV51123
XX ID AAV51123 standard; DNA; 41 BP.
XX
XX AAV51123;
XX
XX 11-JAN-1999 (first entry)
XX
XX Maize polymorphic marker S27G3/G6-1A DNA.
XX
XX Polymorphic marker; allele-specific; primer; probe; amplification;
XX hybridisation; plant; hybrid certification; genetic contribution;
XX progeny; back-cross; hybrid; ancestry; maize; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
FH variation 21
FT /*tag= "a"
FT /replace= "g"
FT /note= "polymorphism"
XX
XX WO9824796-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US21782.

```

```

XX 07-MAR-1997; 97US-0813507.
XX
XX 02-DEC-1996; 96US-0032069.
XX
XX (AFY-) AFFYMETRIX INC.
XX
XX Landry BS, Lemieux B, Muriigneux A, Sapolsky RJ;
XX
XX WPI; 1998-333252/29.
XX
XX Brassica species allele-specific oligonucleotide probes and primers
XX - useful for plant breeding
XX
XX Claim 1; Page 46; 65pp; English.
XX
XX This DNA sequence is a region of a Zea mays genome which contains a
XX polymorphic marker. This sequence can be used in the construction of
XX allele-specific primers and probes for amplification or hybridisation,
XX e.g. to determine common or disparate ancestry between 2 or more plants,
XX to monitor the genetic contribution of an ancestral plant, to trace the
XX progeny of proprietary plants, in certification of a hybrid plant or to
XX identify the progeny of a back-crossed plant with an ancestral plant.
XX
XX Sequence 41 BP; 8 A; 7 C; 13 G; 13 T; 0 other;
XX
XX Query Match 16.6%; Score 15.4; DB 19; Length 41;
XX Best Local Similarity 66.7%; Pred. No. 3.5e+04;
XX Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX 60 TGTGACTGTGGGCGCTCCAGAAACATTGAGCT 92
XX | | | | | | | | | | | | | | | | | |
XX 8 TGTGACTGTGGGCGCTCCAGACGCTTTTACGT 40
XX
XX RESULT 57
XX AAF30319
XX ID AAF30319 standard; DNA; 44 BP.
XX
XX AAF30319;
XX
XX 14-MAY-2001 (first entry)
XX
XX Cap independent translational enhancer PCR primer.
XX
XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
XX immunotherapy; therapy; tumour; cancer; lymphoma; gene therapy;
XX VRI605; cap independent translational enhancer; CITE; PCR primer;
XX ss.
XX
XX Unidentified.
XX
XX WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI; 2001-123319/13.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
XX polynucleotide and one or more antigen, or cytokine encoding
XX polynucleotides, useful for suppressing tumour growth and for treating
XX autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Example 1; Page 50; 149pp; English.
XX
XX The present sequence is that of a primer used in the PCR

```

CC amplification of a cap independent translation enhancer (CITE)
CC sequence from vector pCITE. The amplified product was used in the
CC construction of generic cloning vector VR1605 (see AAF30339)
CC containing constant regions of the human kappa light chain and
CC gamma 1 heavy chain separated by the CITE sequence. This plasmid
CC is used as a negative control for VR1623 (see AAF30315), a
CC bicistronic chimeric idiotypic vector. Coadministration of VR1623
CC and VR6200 (see AAF30313) encoding a secreted form (see AAB20187)
CC of mouse Fms-like tyrosine kinase (Flt-3 ligand) demonstrated the
CC ability of the invention to enhance protection from tumour
CC challenge in a murine B-cell lymphoma model.

XX Sequence 44 BP; 10 A; 13 C; 8 G; 13 T; 0 other;

Query Match 16.6%; Score 15.4; DB 22; Length 44;
Best Local Similarity 66.7%; Pred. No. 3.6e+04;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

YY 22 GCCTGGTGACATGCTTGTTCACACAT 54
DB 11 GCCTGGTGACATGCTTGTTCACACAT 43

RESULT 58

AAZ68249 standard; DNA; 47 BP.

AC AAZ68249;

DT 10-SEP-2001 (first entry)

DE Human map-related biallelic marker SEQ ID NO:2596.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

FT Key Location/Qualifiers
FT variation replace(24,T)
FT /*tag- a

FT /standard_name="single nucleotide polymorphism"

MO9954500-A2.

PD 28-OCT-1999.

PF 21-APR-1999; 99WO-IB00822.

PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

XX (GEST) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

DR WPI; 2000-013267/01.

PT Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -

PS Claim 3; Page 784; 2745pp: English.

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also

CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.

XX Sequence 47 BP; 18 A; 9 C; 7 G; 13 T; 0 other;

Query Match 16.6%; Score 15.4; DB 21; Length 47;
Best Local Similarity 66.7%; Pred. No. 3.7e+04;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

YY 34 ATGCTTGTTCACATGCAATGATGACT 66
DB 9 ATGCTTGTTCACATGCAATGATGACT 41

RESULT 59

AAZ19908/c standard; cDNA; 29 BP.

AC AAZ19908;

DT 06-DEC-1999 (first entry)

DE Human foetal kidney secreted protein clone pk266_4 probe.

XX Secreted protein; pk266_4; human; therapy; diagnosis; vaccine;
KW probe; ss.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers
FT modified_base 2
FT /*tag- a

FT /note="Biotinylated phosphoramidite residue"

MO9947555-A1.

PD 23-SEP-1999.

PF 18-MAR-1999; 99WO-US05939.

PR 20-MAR-1998; 98US-0078803.

PR 17-MAR-1999; 99US-0078803.

XX (GEMV) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racle LA, Evans C;

PI Merberg D, Treacy M, Agostino KC, Steininger KO;

DR WPI; 1999-562059/47.

PT New polynucleotides derived from murine foetal cell cDNA libraries,
XX potentially used as, e.g. vaccines -

PS Disclosure: Page 105; 107pp: English.

CC This oligonucleotide probe can be used to isolate cDNA clone
CC pk266_4 (see AAZ19908) from composite deposit ATCC 98700. The clone
CC was originally isolated from a human foetal kidney cDNA library.
CC It codes for a novel secreted protein (see AAY31835). The invention
CC provides new human secreted proteins (see AAY31828-38) and
CC polynucleotides (see AAZ19993-901) isolated from foetal cell, adult
CC blood, adult brain and foetal kidney cDNA libraries. They are
CC predicted to have biological activities which would make them
CC suitable for treating, preventing or ameliorating medical
CC conditions in humans and animals, although no supporting data are
CC given. The polynucleotides are also stated to be useful for

CC gene therapy.
 XX
 XX Sequence 29 BP; 8 A; 3 C; 10 G; 7 T; 1 other;
 SQ

Query Match 16.3%; Score 15.2; DB 20; Length 29;
 Best Local Similarity 85.0%; Pred. No. 3.7e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 ATGCGTGGTTCAACACTA 53
 |||||
 DB 25 ATCCCTAGTTCAACACCA 6

RESULT 60
 AAF01570/C
 ID AAF01570 standard; RNA; 29 BP.
 AC AAF01570;
 XX
 XX 16-FEB-2001 (first entry)
 DT
 XX
 XX Hammerhead ribozyme #1561.
 DE
 XX
 XX Ribozyme: erythropoietin; granulocyte colony stimulating factor;
 KM interferon alpha; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200061729-A2.
 PN
 XX
 XX 19-OCT-2000.
 PD
 XX
 XX 11-APR-2000; 2000WO-US09721.
 PF
 XX
 XX 12-APR-1999; 99US-0129390.
 PR
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 XX Blatt L, Zwick M, Pavco P, McSwigen J;
 PI
 XX
 XX WPI: 2000-647423/62.
 DR
 XX
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -
 XX
 XX
 XX Claim 32; Page 91; 164pp; English.
 PS
 XX
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the η 2 Orphan receptor, EARS/COP- η -1, the GATA
 CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 CC
 XX
 XX Sequence 29 BP; 11 A; 5 C; 5 G; 7 U; 1 other;
 SQ

Query Match 16.3%; Score 15.2; DB 21; Length 29;
 Best Local Similarity 69.0%; Pred. No. 3.7e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 59 ATGTGACTGCGGCGCTCAGAAACATT 87
 |||||
 DB 29 ATGTGACTGCGGCTCAGTATAT 1

RESULT 61
 AAS17330
 ID AAS17330 standard; DNA; 33 BP.
 XX
 XX AAS17330;
 AC

XX
 DT 25-FEB-2002 (first entry)
 XX
 XX Overlapping primer #17 for P. gingivalis PG32C high expression.
 DE
 XX
 XX Soluble Porphyromonas gingivalis polypeptide; PG32C; immune response;
 KM periodontitis; gingivitis; periodontal disease; cardiovascular disease;
 KM tooth paste; mouthwash; antibacterial; dental; primer; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX WO200183530-A1.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 27-APR-2001; 2001WO-AU00482.
 PF
 XX
 XX 28-APR-2000; 2000AU-0007182.
 PR
 XX
 XX (CSLC-) CSL LTD.
 PA
 XX
 XX Barr IG, Czajkowski L, Ross BC;
 PI
 XX
 XX WPI: 2002-041482/05.
 DR
 XX
 XX Novel soluble polypeptides comprising fragment of Porphyromonas
 PT gingivalis PG32 and PG33 proteins, useful for eliciting immune response
 PT in subject against P. gingivalis, and for treating or preventing
 PT periodontitis -
 XX
 XX Example 5; Page 34; 55pp; English.
 PS
 XX
 XX The present invention relates to the isolation of soluble
 CC Porphyromonas gingivalis (PG) polypeptides derived from outer membrane
 CC proteins PG32 and PG33, and the polynucleotide sequences encoding
 CC them. The sequences of the invention can be used in compositions
 CC for raising an immune response in a subject against P. gingivalis and
 CC treating, preventing or reducing periodontitis or other P. gingivalis
 CC infections (e.g. gingivitis). Since periodontal disease has linkage with
 CC cardiovascular disease, the polypeptides are also useful for reducing
 CC the incidence or severity of cardiovascular disease or as an adjunct in
 CC treating the cardiovascular disease. An antibody raised against the
 CC polypeptides can be used in oral compositions such as tooth paste,
 CC mouthwash, etc. The polypeptides exhibit improved solubility when
 CC compared to full-length proteins. AAS17314-AAS17337 represent multiple
 CC overlapping oligonucleotide primers used for the generation of PG32C
 CC high expression bias codon replaced DNA.
 CC
 XX
 XX Sequence 33 BP; 7 A; 6 C; 9 G; 11 T; 0 other;
 SQ

Query Match 16.3%; Score 15.2; DB 24; Length 33;
 Best Local Similarity 85.0%; Pred. No. 3.9e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 TTGGTTCAACGATATGCA 58
 |||||
 DB 7 TTGGTTCAACGATATGCA 26

RESULT 62
 AA46356
 ID AA46356 standard; DNA; 36 BP.
 XX
 XX AA46356;
 AC
 XX
 XX 11-NOV-1998 (first entry)
 DT
 XX
 XX PCR primer for serine threonine kinase.
 DE
 XX
 XX Serine threonine kinase; VRK1; VRK2; BIR kinase; cell growth control;
 KM antitumour agent; PCR primer; ss.
 KM
 XX
 XX Synthetic.
 OS

OS Homo sapiens.
 XX MO9829552-A1.
 XX
 PD 09-JUL-1998.
 XX
 PF 25-DEC-1997; 97MO-JP04855.
 XX
 PR 27-DEC-1996; 96JP-0357864.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PI Nezu J, Oku A;
 XX
 DR WPI; 1996-388133/33.
 XX
 PT Serine-threonine kinase highly expressed in actively growing cells -
 PT useful for development of cell growth inhibitors and antitumour
 PT agents
 XX
 PS Example 7; Page 38; 63pp; Japanese.
 CC This sequence is a PCR primer for DNA encoding the serine threonine
 CC kinases of the invention. The two serine threonine kinase variants
 CC (VRK1 and VRK2; shown in AAM64771 and AAM64772 respectively) are highly
 CC expressed in actively growing cells (such as foetal organs), and have
 CC significant homology with the BIR kinase of vaccinia virus. The kinase
 CC can be used as a substrate for the screening of potential inhibitors,
 CC which can then be used in the control of cell growth and as antitumour
 CC agents. Antisense DNA delivered via a suitable vector can also be used
 CC for control of cell growth.
 XX
 SQ Sequence 36 BP; 6 A; 9 C; 14 G; 7 T; 0 other;
 XX
 Query Match 16.3%; Score 15.2; DB 19; Length 36;
 Best Local Similarity 63.9%; Pred. No. 4e+04;
 Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 2 AGCTGGAGACATTCCTGCTGGGTGACAAAGC 37
 Db 1 ACCTGGCGCCGCTGCTGGGTGACAAAGC 36
 XX
 RESULT 63
 AAC64550/C
 ID AAC64550 standard; DNA; 36 BP.
 XX
 AC AAC64550;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Herpesvirus expression vector construction PCR primer P10.
 XX
 KW Herpesvirus; post translational modification; infection; inhibition;
 KW detection; identification; US1.5; phosphorylation site; virucide;
 KW PCR primer; ss.
 XX
 OS Herpesvirus.
 XX
 PN WO200061794-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-US09215.
 XX
 PR 09-APR-1999; 99US-0128500.
 XX
 PA (ARCH-) ARCH DEV CORP.
 XX
 PI Roizman B, Ogile WO;
 XX
 DR WPI; 2000-619232/59.
 XX

PT Assay for detecting inhibitors of herpesvirus infections monitors the
 PT phosphorylation state of polypeptides with a US1.5 phosphorylation site
 PT
 XX
 PS Example 1; Page 91; 143pp; English.
 XX
 CC The present invention describes a screening assay to determine
 CC substances able to inhibit herpesvirus infections. The assay uses a
 CC polypeptide comprising a US1.5 phosphorylation site, a candidate
 CC inhibitor and a kinase and compares the phosphorylation state of the
 CC polypeptide with that of a similar polypeptide contacted with the
 CC kinase in the absence of the candidate inhibitor. The inhibitor of
 CC US1.5 phosphorylation is used to inhibit herpesvirus infection in a
 CC cell before or after the cell is contacted with herpesvirus. In
 CC particular the inhibitor is used to prevent herpes simplex virus
 CC infections. The present sequence represents a PCR primer used in
 CC the construction of herpesvirus expression vectors.
 XX
 SQ Sequence 36 BP; 5 A; 12 C; 9 G; 10 T; 0 other;
 XX
 Query Match 16.3%; Score 15.2; DB 21; Length 36;
 Best Local Similarity 85.0%; Pred. No. 4e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 64 ACTGTCGGCGCTCCAGAAA 83
 Db 28 AATGTCGGCATTCAGAAA 9
 XX
 RESULT 64
 AA168432/C
 ID AA168432 standard; DNA; 36 BP.
 XX
 AC AA168432;
 XX
 DT 14-DEC-2001 (first entry)
 XX
 DE M. organophilum methanol dehydrogenase competitor primer.
 XX
 KW Quantitative determination; high throughput screening; competitor;
 KW amplification; primer; ss.
 XX
 OS Methylobacterium organophilum.
 XX
 PN DE10001881-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 19-JAN-2000; 2000DE-1001881.
 XX
 PR 19-JAN-2000; 2000DE-1001881.
 XX
 PA (UYLE) UNIV LEIPZIG.
 XX
 PI Eschrich K, Rupp S;
 XX
 DR WPI; 2001-603299/69.
 XX
 PT Quantitative determination of nucleic acid, by competitive polymerase
 PT chain reaction in presence of known amount of competitor very similar
 PT to the target -
 XX
 PS Example 4.1; Page 9; 14pp; German.
 CC This invention describes a novel method for quantitative determination of
 CC nucleic acid (I) in a biological sample. A competitive, quantitative
 CC polymerase chain reaction (PCR) is performed using (i) forward and
 CC reverse primers that bind to a fragment of (I) suitable for specific
 CC detection; (ii) a known amount of competitor DNA (Ia), generated in an
 CC earlier PCR, that has the same size and base composition as (I) and
 CC differs only minimally from (I); (iii) usual PCR auxiliaries and (iv) the
 CC sample. The individual strands of both amplicons (from (I) and (Ia)) are
 CC analyzed, directly or after a standard cleavage reaction, for mass and

CC amount, so that they are unequivocally identified from mass and, from
 CC the ratio of their amounts and the known amount of (1a), the amount of
 CC (1) is calculated. The method is used for quantitative determination of
 CC RNA and DNA. The method is simple, quick, automatable and suitable for
 CC high throughput screening. The close similarity between sample and
 CC competitor DNA may eliminate the need for experimental confirmation of
 CC the efficiency of the amplification. This sequence represents a
 CC primer used in the amplification a nucleic acid fragment capable of
 CC acting as a competitor to the Methylolbacterium organophilum methanol
 CC dehydrogenase (MDH) gene used to illustrate the method of the invention.

XX
 SQ Sequence 36 BP; 9 A; 10 C; 11 G; 6 T; 0 other;

Query Match 16.3%; Score 15.2; DB 22; Length 36;
 Best Local Similarity 85.0%; Pred. No. 4e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 TGGGAGCAGCTCCATCTGCC 24
 ||||| ||||| |||||
 DB 21 TGGGAGCCCTCATCTGCC 2

RESULT 65

AAV50773 standard; DNA; 41 BP.

AC AAV50773;

DT 04-JAN-1999 (first entry)

DE Brassica sp. polymorphic marker 85/18A11/86 DNA.

KM Polymorphic marker; allele-specific; primer; probe; amplification;

KW hybridisation; plant; hybrid certification; genetic contribution;

OS Brassica sp.

Key Location/Qualifiers

FT 21
 FT variation
 FT /tag= a
 FT /replace= "g"
 FT /note= "polymorphism"

PN W09824796-A1.

PD 11-JUN-1998.

PF 01-DEC-1997; 97WO-US21782.

PR 07-MAR-1997; 97US-0813507.

PR 02-DEC-1996; 96US-0032069.

PA (AFFY-) AFFYMETRIX INC.

PI Landry BS, Lemieux B, Murrigneux A, Sapolsky RJ;

PT Brassica species allele-specific oligonucleotide probes and primers

PT - useful for plant breeding

PS Claim 1; Page 38; 65pp; English.

XX This DNA sequence is a region of a Brassica napus or Brassica oleracea
 CC genome which contains a polymorphic marker. This sequence can be used
 CC in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution
 CC of an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a
 CC back-crossed plant with an ancestral plant.

SO Sequence 41 BP; 10 A; 11 C; 8 G; 12 T; 0 other;

Query Match 16.3%; Score 15.2; DB 19; Length 41;
 Best Local Similarity 63.9%; Pred. No. 4.2e+04;
 Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 28 GTGACAAATGCTGTTCACACTATCGAATGTG 63
 ||||| ||||| ||||| ||||| |||||
 DB 6 GTGAAAGGCAATGTTCACAAATCTCGCTCGG 41

RESULT 66

ABL96120 standard; DNA; 41 BP.

AC ABL96120;

DT 22-AUG-2002 (first entry)

DE Brassica polymorphic site containing sequence 123-85/18A11/16.

KM Plant; polymorphism; polymorphic; single nucleotide polymorphism; SNP;

KW cruciferae; agriculture; food; canola; condiment; oilseed; vegetable;

OS Brassica sp.

Key Location/Qualifiers

FT 21
 FT variation
 FT /tag= a
 FT /replace= "a"

PN US6358686-B1.

PD 19-MAR-2002.

PF 14-DEC-1999; 99US-0464453.

PR 02-DEC-1996; 96US-032066P.

PA (AFFY-) AFFYMETRIX INC.

PI Lemieux B, Landry BS, Sapolsky RJ;

PT Polymorphic oligonucleotides from Brassica napus and B. oleracea useful

PT for identifying, distinguishing, and determining the relatedness of

PT individual strains or pools of nucleic acids from Cruciferae plants,

PT e.g. canola -

PS Examples; Column 7-8; 40pp; English.

XX The invention relates to oligonucleotides containing polymorphic

CC sequences isolated from two Brassica species, B. napus and B. oleracea,

CC and a method for using them to identify, distinguish, and determine

CC the relatedness of individual strains or pools of nucleic acids from

CC plants within the family Cruciferae. This is useful because many

CC cruciferous plants are important agricultural items and include many

CC foodstuffs, for example, condiments, oilseeds, and vegetables. These

CC include crops such as canola (a type of Brassica napus), which is one of

CC the largest crops in Canada. The sequences given in records ABL96003-
 CC ABL96146 represent oligonucleotides containing polymorphic sequences
 CC isolated from B. napus and B. oleracea.

SO Sequence 41 BP; 10 A; 11 C; 8 G; 12 T; 0 other;

Query Match 16.3%; Score 15.2; DB 24; Length 41;
 Best Local Similarity 63.9%; Pred. No. 4.2e+04;
 Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 28 GTGACAAATGCTGTTCACACTATCGAATGTG 63
 ||||| ||||| ||||| ||||| |||||
 DB 6 GTGAAAGGCAATGTTCACAAATCTCGCTCGG 41

RESULT 67

AA390642
ID AAX90642 standard; DNA; 46 BP.

AC AAX90642;

DT 07-OCT-1999 (first entry)

DE Primer FIV9 to generate pcwFIVdelta17S, packaging expression cassette.

KM FIV9 primer: pcwFIVdelta17S; packaging expression cassette; FIV1;

KM mutagenesis; Sac I; Tth111 I; PF34NDelta17Senv; FIV4;

KM Not I; XhoI; pcwBeta; pcFIVdeltaORF2; ss.

OS Synthetic.

PN WO936511-A2.

PD 22-JUL-1999.

PF 19-JAN-1999; 99WO-US01194.

PR 15-JAN-1999; 99US-0231235.

PR 16-JAN-1998; 98US-0071731.

PR 26-MAY-1998; 98US-0086825.

PR 04-JAN-1999; 99US-0114955.

PA (CHIR) CHIRON CORP.

PI Dubensky TW, Hardy SF, Hsu D, Johnston JC, Sauter SL;

PI Sheridan PL, Yee J;

DX WPI: 1999-444391/37.

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XX

KW cytostatic; virucide; hepatotropic; antinflammatory; antileptic;
 KW antidiabetic; immunosuppressive; nootropic; neuroprotective; cardant;
 KW antibacterial; fungicide; haemostatic; antianemic; anorectic; anti-HIV;
 KW gene therapy; mutagenic; PCR; primer; ss.

OS Feline immunodeficiency virus.

PN WO200242482-A2.

PD 30-MAY-2002.

PF 27-NOV-2001; 2001WO-US44617.

PR 27-NOV-2000; 2000US-253419P.

PA (CHIR) CHIRON CORP.

PI Dubensky TW, Gasmi M, Sauter SL;

PI WPI: 2002-471730/50.

DX

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Example 5; Page 89; 108pp; English.

The invention relates to a chimeric murine leukemia virus (MLV)-feline immunodeficiency virus (FIV) vector construct (I), comprising an MLV vector backbone and an FIV vector construct. (I) is useful for delivering a desired heterologous sequence to a vertebrate or insect e.g. cat, to establish an animal model for studying the parameters of gene delivery in vivo, and also useful in veterinary application. (I) is also useful in therapeutic or productive purposes e.g. for stimulating a specific immune response, inhibiting the interaction of an agent with a host cell receptor, to express a toxic palliative (conditional toxic palliatives), to immunologically regulate the immune system to express markers (phosphatase gene, beta-galactosidase gene or luciferase gene) for replacement gene therapy and/or to produce a recombinant protein. (I) is useful for preventing, inhibiting, stabilizing or reversing infectious, cancerous, autoimmune or immune diseases e.g. viral infections such as human immunodeficiency virus (HIV), hepatitis B virus (HBV), hepatitis C virus (HCV), melanoma, diabetes, graft versus host disease, Alzheimer's disease and heart disease (myocardial infarction), for stimulating an immune response against pathogenic agents such as bacteria, fungi, virus and cancer cells. (I) is involved in inhibiting viral assembly and is useful for treating Gouche's disease, hemophilia, hereditary disorders such as thalassemia, phenylketonuria, cystic fibrosis, Duchenne's muscular dystrophy, emphysema, hypercholesterolemia, hyperlipidemia, anemia, obesity, autoimmune disease, anorexia, inflammation, hepatitis, lentiviral infection. (I) is useful for preventing the spread of metastatic tumour and also for modulating transcription factor activity. Sequences ABL60729-30 represent in vitro mutagenesis primers for constructing a packaging expression cassette pcwFIV17S.

Sequence 46 BP; 6 A; 20 C; 7 G; 12 T; 1 other;

Query Match 16.3%; Score 15.2; DB 24; Length 46;

Best Local Similarity 66.7%; Pred. No. 4.4e+04;

Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

DY 13 CTCGATTCGCTGGGTGACATGCTTGG 42

DB 13 CCCCATCTACTGTTGACGTGCTCCGCG 42

AAZ66988 standard; DNA; 47 BP.

AAZ66988;

10-SEP-2001 (first entry)

OS Synthetic.

XX MO9517911-A1.

XX 06-JUL-1995.

XX 28-DEC-1994; 94WO-US14888.

XX 30-DEC-1993; 93US-0175469.

XX (CELL-) CELL GENESYS INC.

XX Capon DJ, Dubridge RB, Greenburg G, Koller BH, Kucheraipati R,

XX Lourdes Arbones De Rafael M, Smithies O, Williams SR;

XX WPI; 1995-246194/32.

XX Genetically engineered mammalian cells lacking functional MHC
XX antigens - are used to diminish immune attack when used for
XX transplantation and as universal donor cells.

XX Example 4; Page 34; 63pp; English.

XX The sequences represented by AA099205-6 are amplification primers for a
XX probe for a fragment of the human hypoxanthine-guanine-phosphoribosyl
XX transferase (HPT) gene. The probe was used in a southern blot on human
XX retinal pigmented epithelial cell (RPE) DNA. The RPE's used had been
XX targeted for a deletion of part of the HPT gene. The HPT fragment
XX that was being searched for had the neomycin resistance gene inserted
XX into exon 3. The HPT fragment with the insert was contained in the
XX vector HPT.McInnes.ro. This vector was introduced into RPE cells, and
XX the relevant fragment of the HPT gene was replaced by homologous
XX recombination. The probe amplified by these two primers showed that
XX this was the case. This indicates that this method can be used on MHC
XX antigen genes, creating non-immunoreactive cells. Cells containing
XX inactivated MHC genes can be used as donors for transplantation, since
XX they lack markers for host (recipient) immune attack. Transgenic
XX mammals containing the inactivated MHC gene trait can be used in the
XX study of immunodeficiency and may be used as a source of tissues and
XX cells for transplantation.

SQ Sequence 50 BP; 16 A; 10 C; 8 G; 16 T; 0 other;

Query Match 16.3%; Score 15.2; DB 16; Length 50;

Best Local Similarity 71.4%; Pred. No. 4.5e+04;

Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 14 TCCATTCGCGTGGGACATGCTTG 41

DB 48 TCAATTCAGTGTAGAAAATGCTTG 21

RESULT 72

ABK88813 standard; DNA; 15 BP.

XX ABK88813;

XX 07-OCT-2002 (first entry)

XX Adapter oligonucleotide TOPO 3.

XX ss: topoisomerase recognition site; topoisomerase: pCDNAGMDT(sc);

XX pENTR-DT(sc); pCDNA-DEST11; pENTR/D-TOPO; pENTR/SD/TOPO;

XX pCDNA3.2/V5/GMD-TOPO; pCDNA6.2/V5/GMD-TOPO; recombinational cloning;

XX gene targeting; mutation; TOPO 3; adapter.

XX Synthetic.

XX MO200246372-A1.

XX 13-JUN-2002.

PF 07-DEC-2001; 2001WO-US45773.

XX 08-DEC-2000; 2000US-254510P.

XX 11-DEC-2000; 2000US-0732914.

XX 14-SEP-2001; 2001US-318902P.

XX 28-SEP-2001; 2001US-326092P.

XX 27-NOV-2001; 2001US-333124P.

XX (INVT-) INVITROGEN CORP.

XX Chesnut JD, Carrino J, Leong L, Madden K, Gleeson M, Fan J;

XX Brasch MA, Cheo D, Hartley JL, Byrd DRN, Temple GF;

XX WPI; 2002-519662/55.

XX New isolated nucleic acid molecule comprises one or more recombination
XX sites and one or more topoisomerase recognition sites and/or one or
XX more topoisomerases, useful in recombinational cloning

XX Example 5; Page 216; 324pp; English.

XX The invention relates to an isolated nucleic acid molecule (1)
XX comprising: (a) one or more recombination sites; and (b) one or more
XX topoisomerase recognition sites and/or one or more topoisomerases.
XX Also included are a vector comprising the nucleic acid, a vector chosen
XX from pCDNAGMDT(sc), pENTR-DT(sc), pCDNA-DEST11, pENTR/D-TOPO,
XX pENTR/SD/TOPO, pCDNA3.2/V5/GMD-TOPO or pCDNA6.2/V5/GMD-TOPO,
XX a host cell comprising the nucleic acid or vectors and an in vitro method
XX of cloning a nucleic acid molecule involving: (a) obtaining a first
XX nucleic acid molecule to be cloned; (b) mixing the first nucleic acid
XX molecule to be cloned in vitro with a second nucleic acid molecule
XX comprising at least a first topoisomerase recognition site flanked by at
XX least a first recombination site, and at least a second topoisomerase
XX recognition site flanked by at least a second recombination site, where
XX the first and second recombination sites do not recombine with each
XX other, and at least one topoisomerase; and (c) incubating the mixture
XX under conditions such that the first nucleic acid molecule to be cloned
XX is inserted into the second nucleic acid molecule between the first and
XX second topoisomerase recognition sites, thereby producing a first product
XX molecule comprising the first nucleic acid molecule to be cloned between
XX the first and second recombination sites. The method is useful for
XX cloning a nucleic acid molecule. The nucleic acid (1) is useful in
XX methods for recombinational cloning and facilitates construction of gene
XX targeting nucleic acid molecules or vectors which may be used to knockout
XX or mutate a sequence or gene of interest, particularly genes or sequences
XX within a host or host cells such as animal, plant, etc. Thus the
XX nucleic acid is most preferably used for targeting or mutating a sequence
XX of gene. The present sequence is an oligonucleotide used to make an
XX adapter containing a consensus sequence for a topoisomerase site which
XX may be included in the nucleic acid/vectors of the invention.

SQ Sequence 15 BP; 6 A; 4 C; 2 G; 3 T; 0 other;

Query Match 16.1%; Score 15; DB 24; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.6e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAACACTATCGCAAT 60

DB 1 CAACACTATCGCAAT 15

RESULT 73

ABK12602 standard; DNA; 15 BP.

XX ABK12602;

XX 18-JUN-2002 (first entry)

XX Topoisomerase adapter oligonucleotide, TOPO 3.

XX Topoisomerase; recombination; ds.

```

XX Synthetic.
OS
XX
XX W0200216594-A2.
XX
XX 28-FEB-2002.
XX
XX 21-AUG-2001; 2001WO-US26294.
XX
XX 21-AUG-2000; 2000US-226563P.
XX
XX (INV1-) INVITROGEN CORP.
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Chesnut JD, Shuman S, Madden KR, Heyman J, Bennett RP;
XX WPI; 2002-280935/32.
XX
XX Generating directionally linked recombinant nucleic acid molecules by
XX contacting a first double stranded (ds) nucleic-acid molecule with
XX bound topoisomerases at both ends, with a second ds nucleic acid
XX molecule having 2 blunt ends -
XX
XX Example 2; Fig 14; 116pp; English.
XX
XX The invention relates to methods for generating a directionally linked
XX recombinant nucleic acid molecule by contacting a topoisomerase-charged
XX first double stranded (ds) nucleic-acid molecule comprising a first
XX topoisomerase covalently bound at or near a first end, and a second
XX ds nucleic acid molecule comprising a first blunt end and a second
XX end. The method is useful for generating or constructing recombinant
XX nucleic acids, and for covalently linking 2 or more nucleic acid
XX molecules. The present method is simple and more efficient than previous
XX methods for covalently linking nucleic acid sequences. The method greatly
XX reduces the amount of work involved in screening to identify clones
XX containing inserts in the desired orientation by enabling directional
XX cloning efficiencies that are routinely in excess of 90%, and streamlines
XX high throughput gene expression operations and reduces the costs
XX associated with the process. The present sequence represents a
XX topoisomerase adapter oligonucleotide used in the methods of the
XX invention.
XX
XX Sequence 15 BP; 6 A; 4 C; 2 G; 3 T; 0 other;
XX
XX Query Match 16.1%; Score 15; DB 24; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+04;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 46 CAACACTATCGGAAT 60
XX ||||||||||||
XX Db 1 CAACACTATCGGAAT 15
XX
XX RESULT 74
XX AA25796
XX ID AA25796 standard; DNA; 16 BP.
XX
XX AC AA25796;
XX
XX DT 11-JAN-2000 (first entry)
XX
XX DE Expression plasmid construction oligonucleotide #2.
XX
XX KW Yeast; ORF; open reading frame; PCR primer; library; expressible gene;
XX simultaneous manipulation; expression vector; kinase; phosphatase;
XX transcription factor; oncogene; tumour suppressor; ss.
XX
XX OS Synthetic.
XX
XX PN W09951766-A1.
XX
XX PD 14-OCT-1999.

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XX
XX 02-APR-1999; 99WO-US07270.
XX
XX 03-APR-1998; 98US-0054936.
XX
XX (INV1-) INVITROGEN.
XX
XX Fernandez JM, Heyman JA, Hoefler JP, Marks-Hull HL, Sindici MT;
XX WPI; 1999-620212/53.
XX
XX Production of library of expressible coding regions, used for obtaining
XX e.g. kinases, phosphatases, transcription factors, oncogenes or tumor
XX suppressors -
XX
XX Example 3; Page 86; 97pp; English.
XX
XX A method has been developed for producing a library of expressible
XX coding regions. The method comprises: (a) amplifying coding regions
XX using at least one coding region specific primer; (b) inserting each
XX coding region into an expression vector; and (c) verifying the size and
XX orientation of the inserted coding region. The method can be used for
XX the rapid, simultaneous expression of large numbers of gene sequences.
XX It can be used for producing expressible coding regions encoding human
XX proteins such as kinases, phosphatases, transcription factors, oncogenes
XX or tumour suppressors. The present sequence represents an oligonucleotide
XX used in the exemplification of the present invention.
XX
XX Sequence 16 BP; 7 A; 4 C; 2 G; 3 T; 0 other;
XX
XX Query Match 16.1%; Score 15; DB 20; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 3.7e+04;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 46 CAACACTATCGGAAT 60
XX ||||||||||||
XX Db 1 CAACACTATCGGAAT 15
XX
XX RESULT 75
XX ABK96427
XX ID ABK96427 standard; DNA; 29 BP.
XX
XX AC ABK96427;
XX
XX DT 24-SEP-2002 (first entry)
XX
XX DE PCR primer OGR48 for cDNA encoding Discosoma fluorescent protein.
XX
XX KW Coral; fluorescent protein; Anthozoa species; fluorescence emission;
XX fluorescence absorbance; fluorescence resonance energy transfer; FRET;
XX fluorescent labelling; PCR; primer; ss.
XX
XX OS Discosoma sp.
XX
XX W0200242323-A2.
XX
XX PN 30-MAY-2002.
XX
XX PD 22-NOV-2001; 2001WO-EP13604.
XX
XX PR 22-NOV-2000; 2000GB-0028495.
XX
XX PR 22-NOV-2000; 2000US-252790P.
XX
XX PA (DEVG-) DEVGEN NV.
XX
XX PI Nys G, Plaetnick G, Bogaert T;
XX
XX DR WPI; 2002-500276/53.
XX
XX Novel isolated fluorescent protein for producing fluorescence resonance
XX energy transfer for use in in vivo labelling studies, is capable of
XX emitting fluorescence upon irradiation by incident light -

```

XX Example 1; Page 33; 96pp; English.

PS The present invention relates to novel coral fluorescent proteins
CC isolated from two brightly fluorescent Anthozoa species (Polynoa
CC and Discosoma species), and the polynucleotide sequences encoding
CC them. The fluorescent proteins of the invention are capable of
CC emitting fluorescence upon incident light irradiation, where the
CC maximal absorbance of the incident light is 440-480 nm, and maximal
CC fluorescence emission is 470-510 nm. The fluorescent proteins are
CC useful for producing fluorescence resonance energy transfer (FRET),
CC between a donor and acceptor fluorescent protein molecule. The
CC fluorescent proteins are useful for in vivo labelling studies, as
CC a label and/or marker, in particular as a genetic marker and/or
CC expression marker, in the fields of (micro-) biology, biochemistry
CC and/or molecular biology. They are also useful for monitoring
CC expression of proteins within biological systems and subcellular
CC localisation or trafficking of proteins. The polynucleotide
CC sequences encoding the fluorescent proteins are useful for in vitro
CC applications such as hybridisation and/or immunological assays. They
CC are also useful for labelling polypeptides of interest.
CC ABK96395-ABK96461 represent PCR primers used in the examples of the
CC present invention.

XX Sequence 29 BP; 7 A; 8 C; 7 G; 7 T; 0 other;

Query Match 16.1%; Score 15; DB 24; Length 29;
Best Local Similarity 78.3%; Pred. No. 4.5e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 66 NTGCGGCTCCGAAACATTCG 88
DB 1 TCTCAGCATCCGAGACATCG 23

RESULT 76
AAL42596/c
ID AAL42596 standard; DNA; 33 BP.

XX AAL42596;

XX 08-JUL-2002 (first entry)

XX Human dynein receptor similarity kinase 51-26 PCR primer 4.

XX Human; ss; PCR; primer: dynein receptor similarity kinase 51.26; tumour;

XX embryonic developmental deformity; inflammation; orthopaedic disease.

XX Homo sapiens.

XX CN1329155-A.

XX 02-JAN-2002.

XX 21-JUN-2000; 2000CN-0116624.

XX 21-JUN-2000; 2000CN-0116624.

XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

XX Mao Y, Xie Y;

XX WPI; 2002-292823/34.

XX New polypeptide-human dynein receptor similarity kinase 51.26 for

XX treating tumours, embryonic developmental deformity, various

XX inflammations and various orthopaedic diseases -

XX Example 4; Page 20 (Disclosure); 36pp; Chinese.

XX The invention comprises the amino acid and coding sequence of the human

XX dynein receptor similarity kinase 51.26. The dynein receptor similarity

XX kinase, 51.26 DNA and protein sequences are useful for treating tumours,

CC embryonic developmental deformity, inflammations and various orthopaedic

CC diseases. The present DNA sequence represents a PCR primer that is

CC specific for the gene sequence of the human dynein receptor similarity

CC kinase 51.26.

XX Sequence 33 BP; 9 A; 8 C; 9 G; 7 T; 0 other;

Query Match 16.1%; Score 15; DB 24; Length 33;
Best Local Similarity 67.7%; Pred. No. 4.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 AGCACATTCCTCCGCTGACATTCCT 39
DB 32 AGCCCTCATTCCTCGGTATGAGATCAT 2

XX AAX89909/c

XX AAX89909 standard; DNA; 36 BP.

XX 18-OCT-1999 (first entry)

XX Sequence of primer 909-38.

XX Translational repression system; translational repressor; coat protein;

XX constitutive promoter; heterologous gene; bacteriophage MS2; toxic gene;

XX PCR primer; protease gene; ss.

XX Synthetic.

XX Bacteriophage sp.

XX WO938985-A2.

XX 05-AUG-1999.

XX 27-JAN-1999; 99MO-US01725.

XX 26-JAN-1999; 99US-0237712.

XX 28-JAN-1998; 98US-0072794.

XX (AMGE-) AMGEN INC.

XX Brown MC;

XX WPI; 1999-494095/41.

XX A bacteriophage MS2 translational repression system for use in

XX cloning or expressing specific heterologous genes, especially toxic

XX genes

XX Examples; Page 61; 133pp; English.

XX The invention relates to a translational repression system comprising a

XX translational repressor operably linked to a constitutive promoter for

XX use in cloning or expressing a specific heterologous gene. The

XX translational repressor is bacteriophage MS2 coat protein. The improved

XX expression vector systems are capable of expressing exogenous genes,

XX including toxic genes, in Escherichia coli and other host cells. The

XX bacteriophage MS2-based system can be used to stably clone and express

XX certain toxic genes. The MS2-based T4 cassette is useful for the cloning

XX of accessory proteins that are useful in the production of a target

XX protein. The vector systems overcome the problem of promoter leakiness

XX which leads to inappropriate transcription and expression of a gene

XX cloned under the control of the promoter. This can be a problem when

XX cloning toxic genes. The transcriptional control proteins, e.g. mola and

XX asia of bacteriophage T4, regulate transcription and provide a staged

XX inducible promoter system which is much less complicated and more

XX versatile than prior art non-staged systems. T4 middle promoters direct

XX transcription from specific promoters while inhibiting transcription

XX from E. coli promoters, which therefore minimises competition for

CC translational apparatus and inhibits the cell from responding to target
CC protein production by inducing transcription of protease genes.
CC Sequences AAX89905-998 represent PCR primers used in the course of the
CC invention.

XX Sequence 36 BP; 8 A; 8 C; 8 G; 12 T; 0 other;

Query Match 16.1%; Score 15; DB 20; Length 36;
Best Local Similarity 78.3%; Pred. No. 4.8e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GAGCTGGAGCACTCCATTCCTGC 23
DB 35 GAGTTGGAAGAATTCATTCACG 13

RESULT 78

AAX89910
ID AAX89910 standard; DNA; 36 BP.

XX AAX89910;

DT 18-OCT-1999 (first entry)

XX Sequence of primer 909-39.

DE Translational repression system: translational repressor; coat protein;

KW constitutive promoter; heterologous gene; bacteriophage MS2; toxic gene;

KW transcriptional control protein; motif; asid; bacteriophage T4;

KW PCR primer; protease gene; ss.

XX Synthetic.

OS Bacteriophage sp.

XX WO938985-A2.

PN 05-AUG-1999.

XX 27-JAN-1999; 99WO-US01725.

XX 26-JAN-1999; 99US-0237712.

XX 28-JAN-1998; 98US-0072794.

XX (AMGE-) AMGEN INC.

XX Brown WC;

XX WPI; 1999-494095/41.

XX A bacteriophage MS2 translational repression system for use in

XX cloning or expressing specific heterologous genes, especially toxic

XX genes

XX Examples: Page 61; 133pp; English.

XX The invention relates to a translational repression system comprising a

XX translational repressor operably linked to a constitutive promoter for

XX use in cloning or expressing a specific heterologous gene. The

XX translational repressor is bacteriophage MS2 coat protein. The improved

XX expression vector systems are capable of expressing exogenous genes,

XX including toxic genes, in Escherichia coli and other host cells. The

XX bacteriophage MS2-based system can be used to stably clone and express

XX certain toxic genes. The MS2-based T4 cassette is useful for the cloning

XX of accessory proteins that are useful in the production of a target

CC translational apparatus and inhibits the cell from responding to target
CC protein production by inducing transcription of protease genes.
CC Sequences AAX89905-998 represent PCR primers used in the course of the
CC invention.

XX Sequence 36 BP; 11 A; 9 C; 10 G; 6 T; 0 other;

Query Match 16.1%; Score 15; DB 20; Length 36;
Best Local Similarity 78.3%; Pred. No. 4.8e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GAGCTGGAGCACTCCATTCCTGC 23
DB 8 GAGTTGGAAGAATTCATTCACG 30

RESULT 79

AAQ99700/C
ID AAQ99700 standard; DNA; 41 BP.

XX AAQ99700;

DT 26-FEB-1996 (first entry)

XX Bovine respiratory syncytial virus glycoprotein gene PCR primer.

DE Swinepox; vaccine production; genetic engineering; recombinant;

KW vector; antigen; transcription; ss.

XX Bovine respiratory syncytial virus.

XX WO9503070-A1.

XX 02-FEB-1995.

XX 22-JUL-1994; 94WO-US08277.

XX 22-JUL-1993; 93US-0097554.

XX (SYTR) SYNTRO CORP.

XX Cochran MD, Junker DE;

XX WPI; 1995-075025/10.

XX New recombinant swinepox viruses - having foreign DNA inserted into

XX a site which is non-essential for viral replication, used for

XX vaccine prodn.

XX Disclosure: Page 77; 338pp; English.

XX AAQ99699 and AAQ99700 are PCR primers used for the amplification and

XX isolation of the bovine respiratory syncytial virus glycoprotein gene.

XX This gene is used in the construction of homology vector 727-20.5. New

XX recombinant swinepox (SPV) viruses have been made which contain a

XX foreign DNA sequence inserted into a non-essential site of the SPV

XX genome via the use of an homology vector. Homology vector 515-85.1 is

XX a plasmid useful for the insertion of foreign DNA into the SPV genome.

XX The plasmid 515-85.1 contains a unique AclI restriction site into which

XX foreign DNA may be cloned. Recombinant SPVs can be used for immunising

XX an animal against e.g. a human pathogen or equine or bovine pathogen,

XX such as equine influenza A, equine herpes virus 1, bovine respiratory

XX syncytial virus, bovine parainfluenza virus, infectious bursal disease

XX virus or bovine diarrhoea virus. The recombinant viruses are also

CC translational apparatus and inhibits the cell from responding to target
CC protein production by inducing transcription of protease genes.
CC Sequences AAX89905-998 represent PCR primers used in the course of the
CC invention.

XX Sequence 41 BP; 13 A; 12 C; 3 G; 13 T; 0 other;

Query Match 16.1%; Score 15; DB 16; Length 41;
Best Local Similarity 67.7%; Pred. No. 5e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GAGCTGGAGCACTCCATTCCTGC 23
DB 8 GAGTTGGAAGAATTCATTCACG 30

RESULT 79

AAQ99700/C
ID AAQ99700 standard; DNA; 41 BP.

XX AAQ99700;

DT 26-FEB-1996 (first entry)

XX Bovine respiratory syncytial virus glycoprotein gene PCR primer.

DE Swinepox; vaccine production; genetic engineering; recombinant;

KW vector; antigen; transcription; ss.

XX Bovine respiratory syncytial virus.

XX WO9503070-A1.

XX 02-FEB-1995.

XX 22-JUL-1994; 94WO-US08277.

XX 22-JUL-1993; 93US-0097554.

XX (SYTR) SYNTRO CORP.

XX Cochran MD, Junker DE;

XX WPI; 1995-075025/10.

XX New recombinant swinepox viruses - having foreign DNA inserted into

XX a site which is non-essential for viral replication, used for

XX vaccine prodn.

XX Disclosure: Page 77; 338pp; English.

XX AAQ99699 and AAQ99700 are PCR primers used for the amplification and

XX isolation of the bovine respiratory syncytial virus glycoprotein gene.

XX This gene is used in the construction of homology vector 727-20.5. New

XX recombinant swinepox (SPV) viruses have been made which contain a

XX foreign DNA sequence inserted into a non-essential site of the SPV

XX genome via the use of an homology vector. Homology vector 515-85.1 is

XX a plasmid useful for the insertion of foreign DNA into the SPV genome.

XX The plasmid 515-85.1 contains a unique AclI restriction site into which

XX foreign DNA may be cloned. Recombinant SPVs can be used for immunising

XX an animal against e.g. a human pathogen or equine or bovine pathogen,

XX such as equine influenza A, equine herpes virus 1, bovine respiratory

XX syncytial virus, bovine parainfluenza virus, infectious bursal disease

XX virus or bovine diarrhoea virus. The recombinant viruses are also

KW polymorphic site; corn; gramineae species; ss.
 XX Synthetic.
 OS Zea sp.
 XX WO9830717-A2.
 PN 16-JUL-1998.
 PD 02-DEC-1997; 97WO-EP07134.
 PF 02-DEC-1996; 96US-0032069.
 PR (BIOC-) BIOCEN SA.
 PA Murigneux A;
 PI WPI: 1998-399160/34.
 DR
 XX
 PT Vegetal sequences including single nucleotide polymorphism - useful,
 PT e.g. to determine polymorphisms in plants, determine strain in plant
 PT breeding and to correlate polymorphisms with phenotypic traits
 PS
 XX Claim 2; Page 14; 32pp; English.
 CC The present invention describes a nucleic acid segment comprising at
 CC least 10 contiguous nucleotides from a vegetal sequence including a
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
 CC complement of the segment. Also described are: (1) an allele-specific
 CC oligonucleotides hybridizing to segment, or their complements, and (2) a
 CC method of analysing nucleic acids from a subject, by determining if a
 CC base is occupying any one (or a set) of polymorphic sites in 261
 CC sequences derived from six maize lines (see AAV4/7701 to AAV4/7961). The
 CC segments are useful in fingerprint analysis in plants to determine which
 CC polymorphisms are present, which strain a plant belongs to and to
 CC distinguish between strains. The polymorphisms may correlate with
 CC phenotypic traits (e.g. plant growth rate or crop yield), and the
 CC segments are useful to determine the presence/absence of particular
 CC polymorphisms correlating with the existence/absence of specific
 CC traits. The segments are also useful in marker assisted back-cross
 CC techniques to select plants with a higher percentage of recurrent parent
 CC in a back-cross population. Segments incorporate SNPs which occur more
 CC frequently than other polymorphism types and are therefore more likely
 CC to be located close to genetic loci of interest; different forms of
 CC characterised SNPs are also often easier to detect than other
 CC polymorphism types.
 CC
 XX Sequence 41 BP; 7 A; 6 C; 14 G; 13 T; 1 other;
 SQ
 QY
 Db 60 TGTGACTGTGGGCTCCAGAAACATGAGGT 92
 8 TGTGACTGTGGGCTCCAGTGTACAGCTTTACT 40
 Matches 21; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
 Query Match 16.1%; Score 15; DB 19; Length 41;
 Best Local Similarity 63.6%; Pred. No. 5e+04;
 RESULT 83
 AAV26221/C
 ID AAV26221 standard; DNA; 41 BP.
 XX
 AC AAV26221;
 XX
 DT 24-JUL-1998 (first entry)
 XX
 DE BRSV strain 375 (VR-1339) G gene PCR primer from WO9804684.
 XX
 KW Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
 KW pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
 KW Dirofilaria immitis; PCR primer; ss.
 XX
 OS Synthetic.

XX
 PN WO9804684-A1.
 XX
 PD 05-FEB-1998.
 XX
 PF 25-JUL-1997; 97WO-US12212.
 PR 25-JUL-1996; 96US-0686968.
 XX
 PA (SYTR) SYNTRO CORP.
 PI Cochran MD, Junker DE;
 DR WPI: 1998-130677/12.
 XX
 PT Recombinant swine pox virus - useful in vaccine for immunising
 PT animal against swine pox virus
 PS
 XX Disclosure; Page 49; 473pp; English.
 CC The present sequence represents a PCR primer from the present
 CC invention. The present invention specifically describes recombinant
 CC swinepox virus (SPV) comprising a foreign DNA (1) inserted into a
 CC SPV genome which is capable of being expressed in a host cell into
 CC which the virus is introduced, where (1) is inserted into: (a) an
 CC EcoRI site within a region corresponding to a 3.2 kb subfragment of the
 CC HindIII K fragment which contains both a HindIII and an EcoRI site, of
 CC the SPV genome, and optionally (b) an AclI site within a region
 CC corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M
 CC fragment. The recombinant SPV can be used in a vaccine for immunising an
 CC animal against SPV. The invention also provides a method for testing a
 CC swine to determine whether the swine has been vaccinated with the
 CC vaccine, particularly containing S-SPV-008, or is infected with a
 CC naturally occurring wild-type pseudorabies virus. Also (1) inserted into
 CC recombinant SPV can be used in a diagnostic assay, e.g. feline
 CC immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis
 CC p39 and 22kd are useful to detect feline immunodeficiency caused by FIV
 CC and to detect heartworm caused by D. immitis respectively.
 CC
 XX Sequence 41 BP; 13 A; 12 C; 3 G; 13 T; 0 other;
 SQ
 QY
 Db 33 AATGCTGTGCTTCACACATGCGAATCG 63
 40 AATGCTGTGATTTAAGATGATGCGTATGAG 10
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Query Match 16.1%; Score 15; DB 19; Length 41;
 Best Local Similarity 67.7%; Pred. No. 5e+04;
 RESULT 84
 AAA37500
 ID AAA37500 standard; DNA; 41 BP.
 XX
 AC AAA37500;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE Yeast acyltransferase YSCAT2 PCR primer, SEQ ID NO:190.
 XX
 KW Acyltransferase; yeast; lipid synthesis; recombinant expression;
 KW membrane fluidity; cold resistance; transgenic plant;
 KW baculovirus expression; PCR primer; ss.
 XX
 OS Saccharomyces sp.
 XX
 PN WO200018889-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US22231.
 PR 25-SEP-1998; 98US-0101939.

XX (CALJ) CALGENE LLC.
 XX
 XX

PI Lasserer MW, Emig RA, Ruezinsky DM, Van Eenennaam A;
 XX WPI: 2000-303447/26.
 XX

PT Novel acyltransferase related proteins useful for altering membrane
 PT fluidity in plant cells e.g. to induce chill tolerance
 XX
 XX Example 7, Page 32, 126pp, English.

CC The invention relates to nucleic acids encoding novel plant
 CC acyltransferase-like proteins (AA37343-A37445) which comprise one of 8
 CC conserved acyltransferase motifs (AA37343-A37445). Acyltransferases
 CC catalyze the transfer of acyl groups from a donor to a variety of
 CC substrates such as glycerides, sterols, stanols and phosphatides.
 CC Such enzymes play a key role in lipid synthesis, and thereby affect the
 CC characteristics of the plant. For example, cold-hardened plants have
 CC different lipid concentrations in the cell membrane compared to
 CC non-hardened plants, which makes the membrane more fluid and the plant
 CC more tolerant of low temperatures. The nucleic acid sequences of the
 CC proteins in host cells e.g., for recombinant protein production. They
 CC may be expressed in plant cells to alter the lipid composition of the
 CC plant e.g., for the production of chill-resistant plants, or for altering
 CC the composition of plant oils. Sequences AA37495-A37526 represent PCR
 CC primers used in an exemplification of the invention to amplify the yeast
 CC acyltransferase DNAs (AA37527-A37534) for cloning into plant and
 CC baculovirus expression constructs.
 XX

SQ Sequence 41 BP; 11 A; 10 C; 6 G; 14 T; 0 other;

Query Match 16.1%; Score 15; DB 21; Length 41;
 Best Local Similarity 67.7%; Pred. No. 5e+04;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 23 CCTGGTGACATGCTGGTTCACACTA 53
 DB 7 CCTGCAGGTCAATGATTTTTCATCAACA 37

RESULT 85

AA024539
 ID AAD24539 standard; DNA: 41 BP.

AC AAD24539;

DT 07-MAR-2002 (first entry)

DE 12CA5 epitope DNA fragment #2.

XX Chimeric transcription factor; nuclear factor kappaB; NF-kappaB p65;
 KW biological material; biological research; biochemical purification;
 KM transgenic animal; gene therapy; acidic activation motif; ds.
 XX
 OS Unidentified.

Key Location/Qualifiers
 CDS 1..39

FT 1..39
 FT /tag= a
 FT /product= "12CA5 epitope fragment #2"
 FT /note= "CDS does not include start and stop codon"
 FT /partial

PN US6306649-B1.

PD 23-OCT-2001.

PE 27-JUN-1996; 96US-0672213.

PR 27-JUN-1995; 95US-000553P.
 PR 29-DEC-1995; 95US-019614P.

XX (ARIA-) ARIAD GENE THERAPEUTICS INC.
 XX
 XX

PI Gilman MZ, Natesan S;
 XX
 XX

DR WPI: 2002-033255/04.
 DR P-85DB; AAE15354.

PT New recombinant DNA sequence encoding a chimeric transcription factor,
 PT useful in gene therapy by elevating the expression of therapeutic
 PT target gene and allowing expression to reach therapeutically levels -
 XX
 XX Example 1, Column 31-32, 47pp, English.

CC The invention relates to a recombinant DNA sequence encoding a chimeric
 CC transcription factor. The transcription factor comprises one or more
 CC copies of a peptide sequence comprising all or part of a peptide
 CC sequence spanning 361-550 of human nuclear factor (NF)-kappaB p65 and a
 CC peptide sequence heterologous to the sequence selected from VP16 V8, a
 CC VP16 B, VP16 C, HSF or CTF. The recombinant DNA is used for producing
 CC biological materials, in biological researches where precise control
 CC over a target gene is desired, such as in the expression of a protein
 CC or RNA of interest for biochemical purification and in tissue or organ
 CC specific expression of a protein or RNA in transgenic animals to elevate
 CC its biological function. It is also useful in gene therapy strategies by
 CC substantially elevating the expression of therapeutic target gene and
 CC allowing expression factors to reach therapeutically effective levels. The
 CC transcription factors are useful for effecting transcription of target
 CC genes in genetically engineered cells or organisms containing them.
 CC The present sequence is 12CA5 epitope DNA fragment used in the
 CC exemplification of the invention.
 XX

SQ Sequence 41 BP; 16 A; 6 C; 13 G; 6 T; 0 other;

Query Match 16.1%; Score 15; DB 24; Length 41;
 Best Local Similarity 67.7%; Pred. No. 5e+04;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 45 TCACACTATCGGATGCTGCTGCGGCT 75
 DB 5 TCACACTAGAGAGATGCTGCTGCGGCT 35

RESULT 86

AA086970
 ID AAT86970 standard; DNA: 42 BP.

AC AAT86970;

DT 27-MAR-1998 (first entry)

DE Primer used in MHC fusion complex construction.

XX PCR primer; construction; major histocompatibility complex; MHC;
 KW fusion complex; ss.
 XX
 OS Synthetic.

OS Homo sapiens.
 PN WO9728191-A1.

PD 07-AUG-1997.

PE 30-JAN-1997; 97WO-US01617.

PR 31-JAN-1996; 96US-0596387.

PA (DADE-) DADE INT INC.

PI Burkhardt M, Jiao J, Rhode PR, Wong HC;

XX WPI: 1997-402555/37.
 XX

PT Single chain major histocompatibility complex comprising linked
 PT alpha and beta chains - useful for suppressing an immune response
 PT to an auto-immune disease, e.g. multiple sclerosis, rheumatoid
 PT arthritis, diabetes mellitus, etc.
 XX
 PS Example 3; Page 117; 217pp; English.
 CC
 CC The present sequence is a primer used in the construction of major
 CC histocompatibility complex (MHC) fusion complexes.
 XX
 SQ Sequence 42 BP; 6 A; 20 C; 11 G; 5 T; 0 other;
 Query Match 16.1%; Score 15; DB 18; Length 42;
 Best Local Similarity 67.7%; Pred. No. 5e+04;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 11 CACTCATTCTGCTGGTGGACATGCGCTG 41
 DB 1 CCCCCAGGCTTCCCGGGCCACCATGCGCTG 31
 RESULT 87
 AAT74319
 ID AAT74319 standard; DNA; 43 BP.
 XX
 AC AAT74319;
 XX
 DT 03-OCT-1997 (first entry)
 XX
 DE Construct pCGNN-ZFHDL-1FRB fragment DNA.
 XX
 KW Rapamycin; responsive transfected cell; recombinant DNA;
 KW fusion protein; rapamycin binding domain; RBD; FKBP;
 KW FK506-binding protein; FRB domain; genetic engineering; regulation;
 KW transcription; signal transduction; apoptosis; inhibition; virus;
 KW gene therapy; ss.
 XX
 OS Synthetic.
 XX
 FH Location/Qualifiers
 FT 1..43
 FT CDS /tag= a
 FT /product= pCGNN-ZFHDL-1FRB-fragment
 FT 1
 FT misc-feature /tag= b
 FT /note= "ZFHDL fragment that joins this sequence to the
 FT 1..9 5'-end of pCGNN-ZFHDL-1FRB fragment in AAT49028"
 FT misc-feature /label= c
 FT /label= 3'-ZFHDL-fragment
 FT 16..43 /tag= d
 FT /label= 5'-FRB-fragment
 FT 43
 FT misc-feature /tag= e
 FT /note= "FRB fragment that joins this sequence to the
 FT 3'-end of pCGNN-ZFHDL-1FRB fragment in AAT74320"
 XX
 PN W09641865-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09948.
 XX
 PR 09-FEB-1996; 96US-0598776.
 PR 07-JUN-1995; 95US-0481941.
 XX
 PA (ARIA-) ARIAD GENE THERAPEUTICS INC.
 XX
 PI Clackson T, Gilman MZ, Holt DA;
 XX
 DR WPI; 1997-065453/06.
 DR P-PSDB; AAW23604.

XX
 PT New rapamycin-responsive transfected cells - contg. recombinant DNA
 PT encoding fusion proteins which act as biological switches for
 PT regulating biological events
 XX
 PS Example 1; Page 63; 149pp; English.
 CC
 CC The present sequence encodes the pCGNN-ZFHDL-1FRB construct fragment
 CC that contains the 3'-end of ZFHDL and the 5'-end of FRB. The fragment
 CC is attached to AAT49028 by a missing fragment, and is attached to
 CC AAT74320 by another missing fragment which then forms the whole
 CC construct. This is used to produce an animal cell containing at least two
 CC recombinant DNAs. One DNA should encode a chimeric protein which is
 CC capable of binding to rapamycin, or a rapamycin analogue, and comprises
 CC at least one rapamycin binding domain (RBD) and at least one protein
 CC domain heterologous to it; the second recombinant DNA should encode a
 CC second chimeric protein which is capable of forming a complex with
 CC rapamycin, or a rapamycin analogue, and the first chimeric protein and
 CC comprises at least one FKBP:rapamycin binding (FRB) domain and at least
 CC one domain heterologous to it. Contacting these genetically engineered
 CC cells with rapamycin or analogues results in the formation of a complex
 CC (between the fusion proteins, and the rapamycin), and initiation of a
 CC biological response. The products can be used for regulating biological
 CC events such as gene transcription, activation of an intracellular signal
 CC transduction pathway leading to e.g. gene expression or apoptotic cell
 CC death, gene knock-out, blockade of a gene or inhibition of function of a
 CC gene product. They are used particularly for regulated gene therapy and
 CC for production of recombinant proteins and viruses.
 SQ Sequence 43 BP; 16 A; 6 C; 13 G; 6 T; 2 other;
 Query Match 16.1%; Score 15; DB 18; Length 43;
 Best Local Similarity 67.7%; Pred. No. 5.1e+04;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 45 TCACACTATGCGAGATGCGATGCGGCTT 75
 DB 6 TCACACTATGAGAGATGCGATGGAAGGCTT 36
 RESULT 88
 AAY03898
 ID AAY03898 standard; DNA; 45 BP.
 XX
 AC AAY03898;
 XX
 DT 29-APR-1998 (first entry)
 XX
 DE Primer MP16 for chimeric protein construction.
 XX
 KW VZV; varicella-zoster virus; GE glycoprotein; epitope; peptide tag;
 KW chimeric protein; immunodetection; immunoprecipitation; glycoprotein GL;
 KW antibody; PCR primer; amplification; ss.
 XX
 OS Synthetic.
 OS Varicella-zoster virus.
 XX
 PN US5710248-A.
 XX
 PD 20-JAN-1998.
 XX
 PF 29-JUL-1996; 96US-0681935.
 XX
 PR 29-JUL-1996; 96US-0681935.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Grose CF;
 XX
 DR WPI; 1998-109868/10.
 DR
 XX Chimeric protein, useful for immunodetection and immunoprecipitation
 PT - comprising varicella zoster virus glycoprotein GE epitope linked

PT to peptide

PS Example 2; Column 15; 17pp; English.

CC This sequence represents a primer used in the construction of the
CC chimeric protein of the invention. This primer is used to amplify an
CC antigenic fragment of the varicella-zoster virus glycoprotein gE. The
CC chimeric protein is useful for immunodetection and immunoprecipitation,
CC and comprises a protein linked to a heterologous peptide tag having the
CC amino acid sequence shown in AA441061, where the chimeric protein binds
CC to antibody and to the peptide tag. Expressing a recombinant protein
CC (especially VZV glycoprotein gE) as a chimeric protein facilitates its
CC detection and immunopurification.

Sequence 45 BP; 12 A; 9 C; 10 G; 14 T; 0 other;

Query Match 16.1%; Score 15; DB 19; Length 45;

Best Local Similarity 61.5%; Pred. No. 5.1e+04;

Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

DB 30 GACAAAGCCTTGGTTTCAACACTATCGAATGTGACTGT 68

7 GTACCGATTGGCTTGGACAGTATGCGATTGTGATAGT 45

RESULT 89

AA446988 standard; DNA; 45 BP.

AC AA446988;

DT 29-OCT-2001 (first entry)

DE PCR mutagenic primer M16 rev.

KW Chimeric; glycoprotein gE; VZV; peptide tag; immunopurification;

KW Immunoprecipitation; mutagenesis; PCR primer; ss.

OS Synthetic.

OS Varicella-zoster virus.

PN US625462-B1.

PD 03-JUL-2001.

PF 29-SEP-1997; 97US-0939323.

PR 29-JUL-1996; 96US-0681935.

PA (IOWA) UNIV IOWA RES FOUND.

PI Grose CF;

DR WPI; 2001-432078/46.

XX Example 2; Column 15; 18pp; English.

CC The invention relates to a method of isolating a protein that comprises
CC contacting a solution containing a chimeric protein containing a protein
CC linked to one or more heterologous peptide tags and which binds to the
CC antibody to the peptide tag, contacting the antibody solution to the
CC peptide tag, and then isolating the chimeric protein from the solution.
CC A peptide fragment (1) from glycoprotein gE from Varicella zoster virus
CC (VZV) can be used as the peptide tag. The method and (1) are useful in
CC the immunopurification and immunoprecipitation of proteins other than
CC glycoprotein gE (the most abundant protein in the virus envelope). (1)
CC may be used to identify cellular location of the chimeric protein in
CC a cell, to identify the trafficking of the protein through cellular
CC milieu, to detect protein expression in transformed bacteria, as a marker

CC to quantify the level of gene expression from a cell, and to determine

CC protein location within a cell. Antibodies to (1) can be used to test for
CC the presence of the chimeric protein in a eukaryotic cell supernatant,
CC and to identify, isolate, purify and quantify the amount of chimeric
CC protein in a particular column fraction. Sequences AA446983-991 represent
CC primers used for incorporation of the gE 383 epitope into a VZV protein
CC gE by a recombination site specific PCR insertion mutagenesis method.

Sequence 45 BP; 12 A; 9 C; 10 G; 14 T; 0 other;

Query Match 16.1%; Score 15; DB 22; Length 45;

Best Local Similarity 61.5%; Pred. No. 5.1e+04;

Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

DB 30 GACAAAGCCTTGGTTTCAACACTATCGAATGTGACTGT 68

7 GTACCGATTGGCTTGGACAGTATGCGATTGTGATAGT 45

RESULT 90

AA268554 standard; DNA; 47 BP.

AC AA268554;

DT 10-SEP-2001 (first entry)

DE Human map-related biallelic marker SEQ ID NO:2902.

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW genotyping; hybridisation; identification; characterisation;

KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

PN MO9954500-A2.

PD 28-OCT-1999.

PF 21-APR-1999; 99WO-IB00822.

PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

PA (GENSET) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I;

DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome

XX Claim 3; Page 849; 2745pp; English.

CC AA268554 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other

CC treatment.
CC N.B. The SPO ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX

SO Sequence 47 BP; 11 A; 14 C; 7 G; 15 T; 0 other;

Query Match 16.1%; Score 15; DB 21; Length 47;
Best Local Similarity 78.3%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 68 TCGGCGCTCCGAGAAACATTGAG 90
ID 13 TTGTGCTCCATTAATAACTGAG 35

RESULT 91
AAH82220/C
ID AAH82220 standard; DNA; 48 BP.

AC AAH82220;

DE 18-AUG-1999 (first entry)

XX Influenza virus HTCA-A101 gene cloning RT-PCR primer NS+.

XX Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;
KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;
KW vaccine; flu; Influenza; RT-PCR; primer; ss.

XX Synthetic.
OS Influenza virus.

XX WO928445-A1.

XX 10-JUN-1999.

XX 30-NOV-1998; 98WO-KR00384.

XX 29-NOV-1997; 97KR-0064854.

XX (CHEI-) CHEIL JEDANG CORP.

XX Cheoun KH, Kim HG, Kim J, Kim SJ, Lee KH, Seong BL;
PI Yoon JW;

XX WPI; 1999-385377/32.

PT Cold-adapted influenza viruses useful for the production of
PT protective vaccines against flu

PS Example 4; Page 13; 62pp; English.

XX The invention relates to cold-adapted influenza viruses prepared by
CC passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low
CC temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can
CC be selected from a group consisting of PB2 protein gene, PB1 protein
CC gene, PA protein gene, NP protein gene, M protein gene and NS protein
CC gene (AAH82192-X82197). The method is useful for the production of cold-
CC adapted influenza virus that exhibit temperature sensitivity and can be
CC actively grown in fertilized eggs. The virus is useful for vaccines for
CC protection against flu. Live vaccines containing cold-adapted viruses
CC have several advantages over killed vaccines. It can prevent reduction
CC of immunogenicity, which may occur in the killed vaccine where antigenic
CC proteins would be denatured at its inactivation. It can also avoid
CC hypersensitivity due to the prolonged administration of heterologous
CC proteins. It promotes the immunity by inducing IGA and it can be
CC administered into a spray formulation via nasal cavity and thus its
CC application is convenient for children. It is able to inhibit the
CC growth of the wild-type virus and thus its therapeutic effect can be
CC expected. Sequences AAH82198-X82221 represent RT-PCR primers used in the
CC cloning of cold-adapted influenza virus HTCA-A101 gene.
XX

SO Sequence 48 BP; 19 A; 9 C; 13 G; 7 T; 0 other;

Query Match 16.1%; Score 15; DB 20; Length 48;
Best Local Similarity 67.7%; Pred. No. 5.2e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 14 TCCATTCGCTGGGACAAATGCTTGCT 44
ID 46 TCCATTCATGCTTTGTCACCGCTTTGCT 16

RESULT 92
AAI75840
ID AAI75840 standard; DNA; 50 BP.

AC AAI75840;

DE 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:2781.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US27258.

XX 30-NOV-1998; 98US-0168138.

XX 29-NOV-2000; 2000US-0726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -

PS Claim 1; Page 902; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples. The polypeptides encoded by (I) may be used as restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX

SO Sequence 50 BP; 11 A; 11 C; 19 G; 9 T; 0 other;

Query Match 16.1%; Score 15; DB 22; Length 50;
Best Local Similarity 67.7%; Pred. No. 5.3e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 25 TGGGTGACAAATGCTTGTTCACACTATC 55
||||| | | | | | | | | |
DB 20 TGGGTGCCAGGCCAGGTGTGAATTTCTC 50

RESULT 93

AAA26628
ID AAA26628 standard; DNA; 19 BP.

AAA26628;

23-JUN-2000 (first entry)

Human HPC1 mutation screening PCR primer SEQ ID NO:172.

Human; prostate cancer predisposing gene; HPC1; chromosome 1;
susceptibility; tumour suppressor; prostate cancer; cytostatic;
gene therapy; mutant; screening; PCR primer; ss.

Homo sapiens.

W0200012694-A1.

09-MAR-2000.

26-AUG-1999; 99WO-US19508.

26-AUG-1998; 98US-0098183.

(MYRI-) MYRIAD GENETICS INC.

Tavtigian S, Teng DHF, Perry WL, Schroeder MW, Simard J;
Rommens JM;

WPI; 2000-270819/23.

Novel human prostate cancer predisposing gene in which somatic and
germline mutations correlate with prostate cancer, useful in gene
therapy and for diagnosis and prognosis of predisposition to prostate
cancer.

Example 8; Page 73; 159pp; English.

The present invention describes a human prostate cancer susceptibility
gene, designated the human prostate cancer predisposing gene 1 (HPC1).
AAA26455 to AAA26510 represent nucleotide sequences from the HPC1 gene.
The HPC1 gene sequences are used as diagnostic molecules since they
can determine a predisposition to cancers especially, prostate cancer.
Nucleic acid probes from the present invention are used to detect
mismatches of the HPC1 gene or mRNA. Primers from the present invention
can be used for determining the nucleotide sequence of a particular HPC1
allele. The mutations in the HPC1 allele which lead to an altered
function of HPC1 are used in diagnostic and prognostic methods to
determine a predisposition to cancer. HPC1 genes are also used in gene
therapy to treat cancer. The HPC1 gene can be found in the HPC1 region
of human chromosome 1, bound by the markers MM.GAA.158:23.4 and
MM.G57e15.S16. AAA26513 to AAA26521 represent oligonucleotides used in
hybrid selection in an example for the present invention. AAA26522 to
AAA26537 represent PCR primers for the HPC1 gene, and AAA26538 to
AAA26658 represent PCR primers used in mutation screening of the HPC1
gene. AAA26659 to AAA26662 encode the putative protein sequences given in
AAV82362 to AAV82365 from HPC1.

Sequence 19 BP; 3 A; 6 C; 7 G; 3 T; 0 other;

Query Match 15.9%; Score 14.8; DB 21; Length 19;

Best Local Similarity 88.9%; Pred. No. 4.6e+04;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 16 CATTCCTGCTGGGTGACA 33
||| ||||| ||||| |||||
DB 1 CAGCCTGCTGGGTGACA 18

RESULT 94

AA517913/C
ID AA517913 standard; DNA; 21 BP.

AA517913;

12-MAR-2002 (first entry)

Interleukin 18 (IL-18), forward primer for real time PCR.

Interleukin 18; IL-18; cytokine; interleukin-18 inhibitor;
atherosclerosis; cardiant; vasotropic; anti-ather; myocardial infarction;
atherosclerotic plaque; thrombosis of atherosclerotic plaque; stroke;
ischemic syndrome; heart failure; arteriosclerosis; vascularisation;
atheroma; human; real time PCR primer; ss.

Homo sapiens.

W0200185201-A2.

15-NOV-2001.

30-APR-2001; 2001WO-EP04843.

05-MAY-2000; 2000EP-0109606.

(ISMP) ARS APPLIED RES SYSTEMS HOLDING NV.
(INRA) INSERM INST NANT SANTE & RECH MEDICALE.

Chvatchko Y, Tedgui A, Mallat Z;

WPI; 2002-075227/10.

Use of interleukin-18 inhibitor for manufacture of medicament for
treatment and/or prevention of atherosclerosis, thrombosis of
atherosclerotic plaque, atherosclerotic plaque ulcer and heart failure
recurrent events.

Example; Page 28; 54pp; English.

The invention describes the use of interleukin-18 (IL-18) inhibitor for
manufacture of medicament for treatment and/or prevention of diseases or
diseased conditions of the arteries, heart failure recurrent events, or
as diagnostic marker for bad clinical prognosis in heart failure or
recurrent events after first event of heart failure. The IL-18 inhibitor
is useful for: the manufacture of a medicament for treatment and/or
prevention of atherosclerosis/arteriosclerosis; the manufacture of a
medicament for treatment and/or prevention of thrombosis of
atherosclerotic plaque (AP), AP ulcer, AP destabilisation (responsible
for stroke), atheroma, ischemic syndromes e.g. myocardial infarction,
AP disruption or heart failure recurrent events e.g. death, recurrent
ischemia, re-vascularisation and progression of atherosclerosis, where
the heart failure is ischemic or non-ischemic and as a diagnostic
marker for bad clinical prognosis in heart failure or recurrent events
after first event of heart failure. This sequence is the forward primer
for real time PCR, labelled with SYBR green dye (not defined) and used
with the reverse primer AA517912 to measure the quantity of IL-18 in
human atherosclerotic plaque samples, described in the method of the
invention.

Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 other;

Query Match 15.9%; Score 14.8; DB 24; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.8e+04;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 24 CTGGGTGACAAATGCTTGTG 41
||||| ||||| ||||| |||||
DB 18 CTGGGAGACAAATGCTTGTG 1

RESULT 95

AAx72318/C
ID AAX72318 standard; RNA; 27 BP.
XX
AC AAX72318;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme #562.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN W09715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 9; Page 140; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 27 BP; 9 A; 5 C; 4 G; 8 U; 1 other;
XX
Query Match 15.9%; Score 14.8; DB 18; Length 27;
Best Local Similarity 70.4%; Pred. No. 5.2e+04;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 61 GTGACTGTTCGCGCCCTCCAGAAACATT 87
DB 27 GTGACTGTTCCTCATCAGAAACATT 1

RESULT 96
AAX70909/C
ID AAX70909 standard; RNA; 27 BP.
XX
AC AAX70909;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme #581.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX

KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN W09715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 9; Page 114; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 27 BP; 9 A; 5 C; 4 G; 8 U; 1 other;
XX
Query Match 15.9%; Score 14.8; DB 18; Length 27;
Best Local Similarity 70.4%; Pred. No. 5.2e+04;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 61 GTGACTGTTCGCGCCCTCCAGAAACATT 87
DB 27 GTGACTGTTCCTCATCAGAAACATT 1

RESULT 97
AAX27056
ID AAX27056 standard; DNA; 27 BP.
XX
AC AAX27056;
XX
DT 21-MAY-1999 (first entry)
XX
DE Primer for cellobiohydrolase coding sequence.
XX
KW Cellobiohydrolase; CBH A; CBH B; cellulose degradation; food production;
KW beverage production; animal feed production; endoglucanase; PCR primer;
KW ss.
XX
OS Synthetic.
OS Aspergillus niger.
XX
PN W09906574-A1.
XX
PD 11-FEB-1999.
XX

XX MPI; 1999-080963/07.
 DR
 XX
 XX New nucleic acid segments containing polymorphic sites - used for,
 PT e.g. detecting a disease phenotype, in forensics, paternity testing
 PT or genetic mapping of phenotypic traits
 XX
 XX Claim 1; Page 15; 61pp; English.
 PS
 CC Sequences AAX06101-X06558 represent human DNA fragments which contain
 CC biallelic polymorphic markers. The base occupying the polymorphic site
 CC is indicated by the appropriate IUPAC-IUB ambiguity code. These
 CC fragments can be used in a method for determining polymorphic forms in
 CC an individual. The invention further provides computer-readable storage
 CC medium for storing data for access by an application programme being
 CC executed on a data processing system. Such a method comprises a data
 CC structure stored in the computer-readable storage medium, the data
 CC structure including information resident in a database used by the
 CC application programme and including records, each record comprising
 CC information identifying a polymorphism shown in the above sequences. The
 CC products and methods can be used for analysing polymorphic sites in
 CC individuals for testing for the presence of a disease phenotype or in
 CC forensics, paternity testing or genetic mapping of phenotypic traits.
 CC They can also be used for the production of polypeptides expressed by
 CC variant genes and for the production of transgenic animals. The nucleic
 CC acid segments can also be used in the manufacture of medicaments for the
 CC treatment or prophylaxis of diseases.
 XX
 SQ Sequence 31 BP; 8 A; 6 C; 8 G; 8 T; 1 other;
 Query Match 15.9%; Score 14.8; DB 20; Length 31;
 Best Local Similarity 67.9%; Pred. No. 5.4e+04;
 Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 13 CTCGATCTGCTGGTGACATGCTT 40
 ||||| ||||| ||||| |||||
 Db 31 CTCGAGCAGCCAGCTGTGACACTGCTT 4
 RESULT 100
 AAT60552/C
 ID AAT60552 standard; DNA; 36 BP.
 XX
 AC AAT60552;
 XX
 DT 11-JUL-1997 (first entry)
 XX
 DE Progesterin regulated gene 1 (PRG1) reverse primer.
 XX
 KW Progesterin-regulated gene 1; PRG1; breast cancer; tumour; T-47D;
 KW hyperproliferation; metabolic disease; diabetes; cell cycle;
 KW antiproliferative; gene therapy; polymerase chain reaction; PCR;
 KW primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9715674-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 24-OCT-1996; 96MO-AU000669.
 XX
 PR 19-JUL-1996; 96AU-0001128.
 PR 24-OCT-1995; 95AU-0006144.
 XX
 PA (GARV-) GARVAN INST MEDICAL RES.
 XX
 PI Hamilton JA, Watts CKW;
 XX
 DR MPI; 1997-259026/23.
 XX
 PT Progesterin-regulated gene - indicative of a subject's progesterin
 PT responsiveness, also for treatment of metabolic disease or

PT hyperproliferation etc
 XX
 XX Example: Page 14; 50pp; English.
 PS
 XX A forward primer (AAT60551) and reverse primer (AAT60552) were used
 CC to generate a full-length open reading frame of the novel human
 CC progesterin-regulated gene PRG1 (see also AAT60548) contg. terminal
 CC EcoRI and SalI restriction sites. The PCR product was cloned into
 CC bacterial expression vector pTAC-AE-2 to allow prodn. of PRG1
 CC polypeptide (see also AAM15747) as a soluble fusion protein in
 CC Escherichia coli DH5a transformants.
 XX
 SQ Sequence 36 BP; 7 A; 9 C; 10 G; 10 T; 0 other;
 Query Match 15.9%; Score 14.8; DB 18; Length 36;
 Best Local Similarity 88.9%; Pred. No. 5.7e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 73 CCTCAGAAACATTGAG 90
 ||||| ||||| ||||| |||||
 Db 29 CCTCAGAAACACTGAG 12
 Search completed: July 5, 2003, 12:29:25
 Job time : 236 secs

2

GenCore version 5.1.6
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SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 04:25:39 ; Search time 985 Seconds

(without alignments)
2747.778 Million cell updates/sec

Title: US-09-843-377-3_COPY_1000_1092

Perfect score: 93

Sequence: 1 gagctggagcagcctccattc.....ctccagaacattgaggtg 93

Scoring table: IDENTITY NJC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :
GenEmbl: *
1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hgtg_hum: *
31: em_hgtg_iny: *
32: em_hgtg_other: *
33: em_hgtg_mus: *
34: em_hgtg_pln: *
35: em_hgtg_rtd: *
36: em_hgtg_mam: *
37: em_hgtg_vrt: *
38: em_sy: *
39: em_hgtg_hum: *
40: em_hgtg_mus: *
41: em_hgtg_other: *

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Length	DB ID	Description
1	18.6	20.0	45 6	AR078468
2	17.2	18.5	30 6	A11493
3	17	18.3	49 6	AX404630
4	16.8	18.1	50 6	AX159134
5	16.6	17.8	30 6	AR093240
6	16.6	17.8	34 11	C75763
7	16.6	17.8	39 6	I44807
8	16.6	17.8	49 6	I79331
9	16.6	17.8	50 6	AR125663
10	16.6	17.8	50 6	I47075
11	16.4	17.6	47 6	AR149818
12	16.4	17.6	47 6	BD007169
13	16.4	17.6	50 6	AX159152
14	16.2	17.4	40 6	AR078049
15	16.2	17.4	48 9	HSTCR2J
16	16.2	17.4	48 9	S74027
17	16.2	17.2	50 6	AX199602
18	16	17.2	50 9	AE044111
19	15.8	17.0	40 6	AR127202
20	15.8	17.0	42 6	AR109086
21	15.8	17.0	42 6	AR200741
22	15.8	17.0	44 6	I43354
23	15.6	16.8	27 6	AX417271
24	15.6	16.8	33 6	AR022050
25	15.6	16.8	33 6	E27408
26	15.6	16.8	43 6	E202550509
27	15.6	16.8	44 9	AX457962
28	15.6	16.8	50 6	AX157284
29	15.6	16.8	50 6	AX46551
30	15.4	16.6	31 6	A92658
31	15.4	16.6	41 6	AR141007
32	15.4	16.6	43 17	HSMC37D09
33	15.4	16.6	44 6	AX080977
34	15.4	16.3	30 6	A11494
35	15.2	16.3	31 6	AR051493
36	15.2	16.3	31 6	AR072633
37	15.2	16.3	31 6	AR073178
38	15.2	16.3	31 6	AX248615
39	15.2	16.3	15 6	AX468447
40	15	16.1	25 6	I16731
41	15	16.1	31 6	AX249653
42	15	16.1	32 6	AR085045
43	15	16.1	33 6	I16735
44	15	16.1	36 6	AR127205
45	15	16.1	36 6	AR127206
46	15	16.1	41 6	AR019012
47	15	16.1	41 6	AR111609
48	15	16.1	41 6	AR147009
49	15	16.1	41 6	AR158235
50	15	16.1	41 6	AR174250
51	15	16.1	42 6	AR033895
52	15	16.1	42 6	AR175028
53	15	16.1	42 6	AX032460
54	15	16.1	45 6	AR161438
55	15	16.1	45 6	I81454
56	15	16.1	50 6	AX159453
57	15	16.1	21 6	AX301247
58	14.8	15.9	27 6	AR188171
59	14.8	15.9	27 6	AR189580
60	14.8	15.9	27 6	AX000160
61	14.8	15.9	30 6	AR086544
62	14.8	15.9	36 6	AX034592
63	14.8	15.9	36 6	AX407350
64	14.8	15.9	38 6	AX219418
65	14.8	15.9	38 6	AX219418

66	14.8	15.9	41	6	AR200843	AR200843 Sequence	C 139	14.2	15.3	38	23	BD005199	BD005199 Novel yea
67	14.8	15.9	44	6	AR199548	AR199548 Sequence	C 140	14.2	15.3	40	6	AR100696	AR100696 Sequence
68	14.8	15.9	45	6	E06872	E06872 Synthetic D	C 141	14.2	15.3	40	6	AX456210	AX456210 Sequence
69	14.8	15.9	45	6	HS00028	X72133 H. sapiens (C 142	14.2	15.3	40	6	AX456389	AX456389 Sequence
70	14.8	15.9	47	6	A69934	A69934 Sequence 29	C 143	14.2	15.3	42	6	AR200827	AR200827 Sequence
71	14.8	15.9	47	6	AX195022	AX195022 Sequence	C 144	14.2	15.3	43	6	AX483409	AX483409 Sequence
72	14.8	15.9	47	6	BD010500	BD010500 Agents fo	C 145	14.2	15.3	45	6	E21692	E21692 Sequence
73	14.8	15.9	49	1	ACNRRDY8B	AF123886 Coturnix	C 146	14.2	15.3	45	6	AX162316	AX162316 Sequence
74	14.8	15.9	50	5	AF123886	AX157274 Sequence	C 147	14.2	15.3	50	6	AX163871	AX163871 Sequence
75	14.8	15.9	50	6	AX157274	AX003680 Sequence	C 148	14.2	15.3	50	6	AX183561	AX183561 Sequence
76	14.6	15.7	21	6	AX003680	AX003680 Sequence	C 149	14.2	15.3	50	10	MMU041959	MMU041959 Sequence
77	14.6	15.7	21	6	AX118607	AX118607 Sequence	C 150	14.2	15.3	24	6	AX444062	AX444062 Sequence
78	14.6	15.7	30	6	AX11495	AX11495 Nucleotide	C 151	14.2	15.3	24	6	AX444803	AX444803 Sequence
79	14.6	15.7	30	6	AX11499	AX11499 Nucleotide	C 152	14.2	15.3	25	6	AX448032	AX448032 Sequence
80	14.6	15.7	31	6	AX11501	AX055336 Sequence	C 153	14.2	15.3	26	6	AX351726	AX351726 Sequence
81	14.6	15.7	31	6	AR065336	AX395259 Sequence	C 154	14.2	15.3	27	6	AX022989	AX022989 Sequence
82	14.6	15.7	32	6	AX1742	AX1742 Sequence 15	C 155	14.2	15.3	30	6	AX464832	AX464832 Sequence
83	14.6	15.7	33	6	AX1742	AR016271 Sequence	C 156	14.2	15.3	30	6	E25572	E25572 RNA molecu
84	14.6	15.7	35	6	AR016271	AR016273 Sequence	C 157	14.2	15.3	30	6	I30423	I30423 Sequence
85	14.6	15.7	35	6	AR016273	E3562 Vector For	C 158	14.2	15.3	31	6	AX106937	AX106937 Sequence
86	14.6	15.7	39	6	E3562	AR078046 Sequence	C 159	14.2	15.3	31	6	AX137867	AX137867 Sequence
87	14.6	15.7	40	6	AR078046	AR171554 Sequence	C 160	14.2	15.3	31	6	BD002507	BD002507 Gene comp
88	14.6	15.7	40	6	AR171554	AR209865 Sequence	C 161	14.2	15.3	33	6	I11436	I11436 Sequence 6
89	14.6	15.7	40	6	AR209865	AX201867 Sequence	C 162	14.2	15.3	33	6	AX359903	AX359903 Sequence
90	14.6	15.7	40	6	AX201867	185801 Sequence 9	C 163	14.2	15.3	34	6	AX359903	AX359903 Sequence
91	14.6	15.7	45	6	185801	AR003527 Sequence	C 164	14.2	15.3	35	6	AX359903	AX359903 Sequence
92	14.6	15.7	45	6	AR003527	AX201009 Sequence	C 165	14.2	15.3	35	6	AX359903	AX359903 Sequence
93	14.6	15.7	45	6	AX201009	AX267808 Sequence	C 166	14.2	15.3	35	6	AX359903	AX359903 Sequence
94	14.6	15.7	45	6	AX267808	155640 Sequence 4	C 167	14.2	15.3	36	6	AR144725	AR144725 Sequence
95	14.6	15.7	45	6	155640	X81548 H. sapiens r	C 168	14.2	15.3	36	6	AR022556	AR022556 Sequence
96	14.6	15.7	45	6	HSCEHL13	AR052850 Sequence	C 169	14.2	15.3	42	6	E03621	E03621 DNA primer
97	14.6	15.7	47	6	AR052850	EL1564 Oligonucleo	C 170	14.2	15.3	43	6	AR013883	AR013883 Sequence
98	14.6	15.7	48	6	E16564	113622 Sequence 7	C 171	14.2	15.3	43	6	AR033837	AR033837 Sequence
99	14.6	15.7	48	6	I13622	163473 Sequence 4	C 172	14.2	15.3	43	6	AR042497	AR042497 Sequence
100	14.6	15.7	48	6	163473	E3566 Vector for	C 173	14.2	15.3	43	6	AR058377	AR058377 Sequence
101	14.6	15.7	49	6	E3566	AR152855 Sequence	C 174	14.2	15.3	43	6	149593	149593 Sequence
102	14.6	15.7	49	6	AR152855	AX356511 Sequence	C 175	14.2	15.3	43	6	I74290	I74290 Sequence
103	14.6	15.7	49	6	AR152855	AX444128 Sequence	C 176	14.2	15.3	46	6	AR089103	AR089103 Sequence
104	14.6	15.7	20	6	AX444128	AX448096 Sequence	C 177	14.2	15.3	46	6	I06580	I06580 Sequence
105	14.6	15.7	20	6	AX48096	E26684 Improved me	C 178	14.2	15.3	47	6	AX194945	AX194945 Sequence
106	14.6	15.7	24	6	E26684	A64575 Sequence 2	C 179	14.2	15.3	48	6	AX286811	AX286811 Sequence
107	14.6	15.7	25	6	A64575	A64575 Sequence 3	C 180	14.2	15.3	48	6	AX286863	AX286863 Sequence
108	14.6	15.7	26	6	AR059492	AR059492 Sequence	C 181	14.2	15.3	48	6	149599	149599 Sequence
109	14.6	15.7	29	6	I56676	I56676 Sequence 2	C 182	14.2	15.3	49	6	AR211693	AR211693 Sequence
110	14.6	15.7	32	6	AR059492	AR003503 Sequence	C 183	14.2	15.3	49	6	HMTCVDL1E2	HMTCVDL1E2 Sequence
111	14.6	15.7	32	6	I56676	A46307 Sequence 5	C 184	14.2	15.3	50	6	AR050768	AR050768 Sequence
112	14.6	15.7	40	6	A46307	AX107167 Sequence	C 185	14.2	15.3	50	6	AR060452	AR060452 Sequence
113	14.6	15.7	43	6	AR0188	AX286225 Sequence	C 186	14.2	15.3	50	6	AR062213	AR062213 Sequence
114	14.6	15.7	46	6	AX286225	AR168818 Sequence	C 187	14.2	15.3	50	6	BD003242	BD003242 P-Selecti
115	14.6	15.7	47	6	AR200287	AR200287 Sequence	C 188	14.2	15.3	50	6	AF071627	AF071627 Mus muscu
116	14.6	15.7	47	6	I27812	I27812 Sequence 44	C 189	14.2	15.3	19	6	A24033	A24033 Synthetic m
117	14.6	15.7	48	6	A27635	AX234385 Sequence	C 190	14.2	15.3	20	6	AR212073	AR212073 Sequence
118	14.6	15.7	48	6	AX234385	AR128848 Sequence	C 191	14.2	15.3	20	6	AX295875	AX295875 Sequence
119	14.6	15.7	47	6	AR168818	101078 Sequence 4	C 192	14.2	15.3	20	6	AX348015	AX348015 Sequence
120	14.6	15.7	47	6	AR200287	104579 Sequence 9	C 193	14.2	15.3	21	6	116826	116826 Sequence 4
121	14.6	15.7	48	6	A27635	A84755 Sequence 7	C 194	14.2	15.3	21	6	AX289945	AX289945 Sequence
122	14.6	15.7	48	6	AX234385	AR18433 Sequence	C 195	14.2	15.3	24	6	AX291242	AX291242 Sequence
123	14.6	15.7	48	6	AX234385	AX455420 Sequence	C 196	14.2	15.3	25	6	AX440933	AX440933 Sequence
124	14.6	15.7	49	6	AR123848	AR109657 Sequence	C 197	14.2	15.3	26	6	AX033455	AX033455 Sequence
125	14.6	15.7	49	6	I01078	AR016579 Sequence	C 198	14.2	15.3	26	6	E55468	E55468 Gene expres
126	14.6	15.7	20	6	I04579	AR106416 Sequence	C 199	14.2	15.3	30	6	AR151209	AR151209 Sequence
127	14.6	15.7	20	6	AR18433	AR016579 Sequence	C 200	14.2	15.3	31	6	AR18385	AR18385 Sequence
128	14.6	15.7	26	6	AR3430	AR093242 Sequence	C 201	14.2	15.3	31	6	AX023018	AX023018 Sequence
129	14.6	15.7	27	6	AR109657	AR016579 Sequence	C 202	14.2	15.3	31	6	AX100939	AX100939 Sequence
130	14.6	15.7	28	6	AR106416	AR093242 Sequence	C 203	14.2	15.3	33	6	AR069587	AR069587 Sequence
131	14.6	15.7	28	6	AR093242	AX247975 Sequence	C 204	14.2	15.3	33	6	AR138393	AR138393 Sequence
132	14.6	15.7	31	6	AX247975	AX402768 Sequence	C 205	14.2	15.3	35	6	AX463190	AX463190 Sequence
133	14.6	15.7	31	6	AX402768	AX420105 Sequence	C 206	14.2	15.3	35	11	C75754	C75754 Homo sapien
134	14.6	15.7	33	6	AX420105	AR093233 Sequence	C 207	14.2	15.3	36	6	AR150990	AR150990 Sequence
135	14.6	15.7	35	6	AR093233	BD012651 Novel yea	C 208	14.2	15.3	36	6	AR156060	AR156060 Sequence
136	14.6	15.7	35	6	BD012651		C 209	14.2	15.3	36	6		
137	14.6	15.7	38	6			C 210	14.2	15.3	36	6		
138	14.6	15.7	38	6			C 211	14.2	15.3	36	6	HMTCVDL1D	HMTCVDL1D Sequence

212	13.8	14.8	37	6	AX183799	AX183799 Sequence	C 285	13.4	14.4	25	6	116733	116733 Sequence 10
C 213	13.8	14.8	38	6	A97235	A97235 Sequence 81	C 286	13.4	14.4	26	6	AR054525	AR054525 Sequence
214	13.8	14.8	41	6	A27378	A27378 Oligonucleo	C 287	13.4	14.4	28	6	AR011828	AR011828 Sequence
215	13.8	14.8	41	6	I27575	I27575 Sequence 89	C 288	13.4	14.4	28	6	AR090370	AR090370 Sequence
216	13.8	14.8	42	5	CHKCA218	J00813 chicken alp	C 289	13.4	14.4	28	6	AR197405	AR197405 Sequence
217	13.8	14.8	44	6	AX327572	AX327572 Sequence	C 290	13.4	14.4	28	6	E04876	E04876 Synthetic D
218	13.8	14.8	45	6	AX061875	AX061875 Sequence	C 291	13.4	14.4	28	6	I16736	I16736 Sequence 13
219	13.8	14.8	45	9	S77758	S77758 Homo sapien	C 292	13.4	14.4	28	6	I77151	I77151 Sequence 23
C 220	13.8	14.8	46	6	AR032523	AR032523 Sequence	C 293	13.4	14.4	30	6	A39985	A39985 Sequence 6
C 221	13.8	14.8	46	6	AR209187	AR209187 Sequence	C 294	13.4	14.4	30	6	AR021166	AR021166 Sequence
C 222	13.8	14.8	46	6	AX116725	AX116725 Sequence	C 295	13.4	14.4	30	6	E11954	E11954 Primer, 9/1
C 223	13.8	14.8	46	6	E07977	E07977 Pr.Lmer, 9/1	C 296	13.4	14.4	30	6	E33951	E33951 Method for
C 224	13.8	14.8	46	6	I29263	I29263 Sequence 13	C 297	13.4	14.4	31	6	AR013817	AR013817 Sequence
C 225	13.8	14.8	46	6	I90937	I90937 Sequence 13	C 298	13.4	14.4	31	6	AR033771	AR033771 Sequence
C 226	13.8	14.8	47	6	AX441347	AX441347 Sequence	C 299	13.4	14.4	31	6	AR042431	AR042431 Sequence
C 227	13.8	14.8	48	6	AX322177	AX322177 Sequence	C 300	13.4	14.4	31	6	AR058311	AR058311 Sequence
C 228	13.8	14.8	49	6	AX356710	AX356710 Sequence	C 301	13.4	14.4	31	6	AR069594	AR069594 Sequence
C 229	13.8	14.8	49	6	AX356711	AX356711 Sequence	C 302	13.4	14.4	31	6	AR088137	AR088137 Sequence
C 230	13.8	14.8	50	6	I08627	I08627 Sequence 28	C 303	13.4	14.4	31	6	AR102927	AR102927 Sequence
C 231	13.6	14.6	20	6	AR137527	AR137527 Sequence	C 304	13.4	14.4	31	6	AR1119573	AR1119573 Sequence
C 232	13.6	14.6	20	6	AR139033	AR139033 Sequence	C 305	13.4	14.4	31	6	I21881	I21881 Sequence 7
C 233	13.6	14.6	20	6	AR147500	AR147500 Sequence	C 306	13.4	14.4	31	6	I23309	I23309 Sequence 7
C 234	13.6	14.6	20	6	AR150392	AR150392 Sequence	C 307	13.4	14.4	31	6	I63585	I63585 Sequence 7
C 235	13.6	14.6	25	6	A67701	A67701 Sequence 31	C 308	13.4	14.4	33	6	A41741	A41741 Sequence 14
C 236	13.6	14.6	26	6	A00918	A00918 Nucleotide	C 309	13.4	14.4	33	9	HSB249313	HSB249313 Homo sapi
C 237	13.6	14.6	26	6	AX487958	AX487958 Sequence	C 310	13.4	14.4	34	6	AR029115	AR029115 Sequence
C 238	13.6	14.6	28	6	A00919	A00919 Nucleotide	C 311	13.4	14.4	34	6	AR087132	AR087132 Sequence
C 239	13.6	14.6	28	6	AX306343	AX306343 Sequence	C 312	13.4	14.4	34	6	AR065927	AR065927 Sequence
C 240	13.6	14.6	29	6	AX183709	AX183709 Sequence	C 313	13.4	14.4	34	6	AR111489	AR111489 Sequence
C 241	13.6	14.6	31	6	AX467191	AX467191 Sequence	C 314	13.4	14.4	35	6	A58324	A58324 Sequence 2
C 242	13.6	14.6	32	6	AR085044	AR085044 Sequence	C 315	13.4	14.4	35	6	A92324	A92324 Sequence 4
C 243	13.6	14.6	34	6	A28091	A28091 Human GABA	C 316	13.4	14.4	35	6	AR105322	AR105322 Sequence
C 244	13.6	14.6	34	6	A39288	A39288 Sequence 13	C 317	13.4	14.4	35	6	AX337940	AX337940 Sequence
C 245	13.6	14.6	34	6	I98869	I98869 Sequence 3	C 318	13.4	14.4	35	6	BD009956	BD009956 Retrovira
C 246	13.6	14.6	35	6	A0361	A0361 Artificial	C 319	13.4	14.4	36	6	A19271	A19271 Oligonucleo
C 247	13.6	14.6	36	6	AR004910	AR004910 Sequence	C 320	13.4	14.4	36	6	AR025354	AR025354 Sequence
C 248	13.6	14.6	36	6	AR020592	AR020592 Sequence	C 321	13.4	14.4	38	6	AX009607	AX009607 Sequence
C 249	13.6	14.6	38	6	AX228664	AX228664 Sequence	C 322	13.4	14.4	39	1	AFU430249	AFU430249 Archaeogl
C 250	13.6	14.6	39	6	AR152469	AR152469 Sequence	C 323	13.4	14.4	39	6	AX230516	AX230516 Sequence
C 251	13.6	14.6	39	6	AX463052	AX463052 Sequence	C 324	13.4	14.4	39	6	I49796	I49796 Sequence 20
C 252	13.6	14.6	41	6	A01533	A01533 Joining reg	C 325	13.4	14.4	40	6	AR182157	AR182157 Sequence
C 253	13.6	14.6	41	6	AR009885	AR009885 Sequence	C 326	13.4	14.4	40	6	I15929	I15929 Sequence 30
C 254	13.6	14.6	41	6	AR141014	AR141014 Sequence	C 327	13.4	14.4	40	6	I15947	I15947 Sequence 48
C 255	13.6	14.6	42	6	AR032564	AR032564 Sequence	C 328	13.4	14.4	40	6	I16128	I16128 Sequence 30
C 256	13.6	14.6	42	6	AX209228	AX209228 Sequence	C 329	13.4	14.4	40	6	I16146	I16146 Sequence 48
C 257	13.6	14.6	42	6	AX411731	AX411731 Sequence	C 330	13.4	14.4	41	6	AX046598	AX046598 Sequence
C 258	13.6	14.6	42	6	AX411732	AX411732 Sequence	C 331	13.4	14.4	41	6	AX395247	AX395247 Sequence
C 259	13.6	14.6	42	6	I29304	I29304 Sequence 17	C 332	13.4	14.4	41	6	I65505	I65505 Sequence 1
C 260	13.6	14.6	42	6	I90978	I90978 Sequence 17	C 333	13.4	14.4	41	11	AL806208	AL806208 Arabidops
C 261	13.6	14.6	42	9	HSTCELG	X58163 Human T-cell	C 334	13.4	14.4	42	6	AR023974	AR023974 Sequence
C 262	13.6	14.6	42	9	SR0775	SR0775 gamma delta	C 335	13.4	14.4	42	6	AR054711	AR054711 Sequence
C 263	13.6	14.6	43	6	AR078827	AR078827 Sequence	C 336	13.4	14.4	42	6	AR061707	AR061707 Sequence
C 264	13.6	14.6	44	6	A00921	A00921 Nucleotide	C 337	13.4	14.4	42	6	AR061948	AR061948 Sequence
C 265	13.6	14.6	45	6	AR075912	AR075912 Sequence	C 338	13.4	14.4	42	6	AR063649	AR063649 Sequence
C 266	13.6	14.6	45	6	AR083198	AR083198 Sequence	C 339	13.4	14.4	42	6	AR086130	AR086130 Sequence
C 267	13.6	14.6	45	6	AX405393	AX405393 Sequence	C 340	13.4	14.4	42	6	AR089560	AR089560 Sequence
C 268	13.6	14.6	45	6	AX452932	AX452932 Sequence	C 341	13.4	14.4	42	6	AR093645	AR093645 Sequence
C 269	13.6	14.6	45	6	AX452934	AX452934 Sequence	C 342	13.4	14.4	42	6	AR13584	AR13584 Sequence
C 270	13.6	14.6	45	6	I20781	I20781 Sequence 5	C 343	13.4	14.4	42	6	AR206182	AR206182 Sequence
C 271	13.6	14.6	46	6	AX076970	AX076970 Sequence	C 344	13.4	14.4	42	6	I24104	I24104 Sequence 19
C 272	13.6	14.6	47	6	A01758	A01758 Plasmid pgb	C 345	13.4	14.4	42	6	I18592	I18592 Sequence 19
C 273	13.6	14.6	47	6	AX194956	AX194956 Sequence	C 346	13.4	14.4	42	6	I14804	I14804 Sequence 28
C 274	13.6	14.6	48	9	HSBTCRV28	Z27206 H.sapiens r	C 347	13.4	14.4	42	6	I76147	I76147 Sequence 19
C 275	13.6	14.6	50	6	A79779	A79779 Sequence 6	C 348	13.4	14.4	42	9	S79063	S79063 T-cell rece
C 276	13.6	14.6	50	6	AR018109	AR018109 Sequence	C 349	13.4	14.4	43	10	RATRRAR01	RATRRAR01
C 277	13.4	14.4	20	6	AR172893	AR172893 Sequence	C 350	13.4	14.4	43	14	DB8820	DB8820 Hepatis G
C 278	13.4	14.4	24	12	AB069166	AB069166 Synthetic	C 351	13.4	14.4	44	6	AR069636	AR069636 Sequence
C 279	13.4	14.4	25	6	AR106305	AR106305 Sequence	C 352	13.4	14.4	44	6	E41645	E41645 Antibody ag
C 280	13.4	14.4	25	6	AR126275	AR126275 Sequence	C 353	13.4	14.4	45	6	A27633	A27633 JGV coat p
C 281	13.4	14.4	25	6	AX207016	AX207016 Sequence	C 354	13.4	14.4	46	6	AR129962	AR129962 Sequence
C 282	13.4	14.4	25	6	AX327795	AX327795 Sequence	C 355	13.4	14.4	46	6	AR139127	AR139127 Sequence
C 283	13.4	14.4	25	6	AX347645	AX347645 Sequence	C 356	13.4	14.4	46	6	AR151104	AR151104 Sequence
C 284	13.4	14.4	25	6	AX377032	AX377032 Sequence	C 357	13.4	14.4	46	6	AR205074	AR205074 Sequence

C 358	13.4	14.4	47	6	AR013902	AR013902 Sequence	C 431	13.2	14.2	35	6	I56886	I56886 Sequence 14
C 359	13.4	14.4	47	6	AR033856	AR033856 Sequence	C 432	13.2	14.2	35	6	I70361	I70361 Sequence 15
C 360	13.4	14.4	47	6	AR042516	AR042516 Sequence	C 433	13.2	14.2	35	6	I70376	I70376 Sequence 14
C 361	13.4	14.4	47	6	AR058396	AR058396 Sequence	C 434	13.2	14.2	35	6	I86387	I86387 Sequence 15
C 362	13.4	14.4	47	6	AR088222	AR088222 Sequence	C 435	13.2	14.2	36	6	AX100930	AX100930 Sequence
C 363	13.4	14.4	47	6	AX194670	AX194670 Sequence	C 436	13.2	14.2	36	6	AX391162	AX391162 Sequence
C 364	13.4	14.4	47	6	AX195027	AX195027 Sequence	C 437	13.2	14.2	36	6	AX399487	AX399487 Sequence
C 365	13.4	14.4	47	10	MUSIGHY	M22391 Mouse Ig ge	C 438	13.2	14.2	37	1	ECORRG08	AX1114 E.coli 235
C 366	13.4	14.4	47	10	MUSIGHY	M22392 Mouse Ig ge	C 439	13.2	14.2	38	6	AT6311	AT6311 Sequence 17
C 367	13.4	14.4	48	6	AR122070	AR122070 Sequence	C 440	13.2	14.2	38	6	AR6351	AR6351 Sequence 25
C 368	13.4	14.4	48	6	AR122070	AR122070 Sequence	C 441	13.2	14.2	38	6	AR166165	AR166165 Sequence
C 369	13.4	14.4	48	6	AX221568	AX221568 Sequence	C 442	13.2	14.2	38	6	AR200023	AR200023 Sequence
C 370	13.4	14.4	48	6	AX222154	AX222154 Sequence	C 443	13.2	14.2	38	6	AX220209	AX220209 Sequence
C 371	13.4	14.4	48	6	AX223762	AX223762 Sequence	C 444	13.2	14.2	38	6	BD004256	BD004256 Method fo
C 372	13.4	14.4	48	6	AX274437	AX274437 Sequence	C 445	13.2	14.2	38	6	E33230	E33230 Novel metha
C 373	13.4	14.4	49	9	HSU030391	AX357197 Sequence	C 446	13.2	14.2	39	6	AX367159	AX367159 Sequence
C 374	13.4	14.4	50	6	AX147194	U30391 Human Isola	C 447	13.2	14.2	40	6	AX456323	AX456323 Sequence
C 375	13.4	14.4	50	6	AX161126	AX147194 Sequence	C 448	13.2	14.2	42	6	I06669	I06669 Sequence 12
C 376	13.4	14.4	50	6	AX165014	AX161126 Sequence	C 449	13.2	14.2	42	6	I50914	I50914 Sequence 3
C 377	13.4	14.4	50	6	AX189995	AX165014 Sequence	C 450	13.2	14.2	43	6	MMRE3RNA	MMRE3RNA
C 378	13.4	14.4	50	6	AX189997	AX189995 Sequence	C 451	13.2	14.2	43	6	AR08053	AR08053
C 379	13.4	14.4	50	6	AX189997	AX189997 Sequence	C 452	13.2	14.2	43	6	AX13206	AX13206
C 380	13.4	14.4	50	9	HUMTCV770	L39537 Homo sapien	C 453	13.2	14.2	43	6	AR033998	AR033998
C 381	13.4	14.4	50	14	ACRCJ	K01622 Reticuloend	C 454	13.2	14.2	43	6	AR124007	AR124007
C 382	13.4	14.2	18	6	AR084734	AR084734 Sequence	C 455	13.2	14.2	43	6	AX428332	AX428332
C 383	13.2	14.2	20	6	AR098934	AR098934 Sequence	C 456	13.2	14.2	43	6	BD011776	BD011776
C 384	13.2	14.2	20	6	AR150278	AR150278 Sequence	C 457	13.2	14.2	43	6	BD011777	BD011777
C 385	13.2	14.2	20	6	BD012462	BD012462 A novel g	C 458	13.2	14.2	43	6	HSU04005	HSU04005
C 386	13.2	14.2	20	6	I79774	I79774 Sequence 70	C 459	13.2	14.2	43	6	BD004173	BD004173
C 387	13.2	14.2	20	23	BD008129	BD008129 A novel g	C 460	13.2	14.2	43	23	BD004174	BD004174
C 388	13.2	14.2	21	6	AR178622	AR178622 Sequence	C 461	13.2	14.2	44	9	HUMRPL112	HUMRPL112
C 389	13.2	14.2	21	6	AR182144	AR182144 Sequence	C 462	13.2	14.2	45	6	A26474	A26474
C 390	13.2	14.2	21	6	AX088192	AX088192 Sequence	C 463	13.2	14.2	45	8	YSCENC163	YSCENC163
C 391	13.2	14.2	21	6	E51395	E51395 Method for	C 464	13.2	14.2	46	6	I06670	I06670
C 392	13.2	14.2	22	6	AX418163	AX418163 Sequence	C 465	13.2	14.2	47	6	AX114370	AX114370
C 393	13.2	14.2	22	6	E05344	E05344 Type 1 Mare	C 466	13.2	14.2	47	6	BD011798	BD011798
C 394	13.2	14.2	24	6	AX015313	AX015313 Sequence	C 467	13.2	14.2	47	9	HUM01688A	HUM01688A
C 395	13.2	14.2	24	6	AX488071	AX488071 Sequence	C 468	13.2	14.2	47	23	BD004195	BD004195
C 396	13.2	14.2	25	6	AR090393	AR090393 Sequence	C 469	13.2	14.2	47	23	BD004196	BD004196
C 397	13.2	14.2	25	6	AR197428	AR197428 Sequence	C 470	13.2	14.2	48	6	A25736	A25736
C 398	13.2	14.2	26	6	BD012014	BD012014 Hydroceph	C 471	13.2	14.2	48	6	AR051408	AR051408
C 399	13.2	14.2	26	6	E55063	E55063 Hydroceph	C 472	13.2	14.2	48	6	AR075919	AR075919
C 400	13.2	14.2	26	23	BD004494	BD004494 Hydroceph	C 473	13.2	14.2	48	6	AR083205	AR083205
C 401	13.2	14.2	27	6	AR091132	AR091132 Sequence	C 474	13.2	14.2	48	6	AX207217	AX207217
C 402	13.2	14.2	27	6	AR198167	AR198167 Sequence	C 475	13.2	14.2	48	6	AX357194	AX357194
C 403	13.2	14.2	28	6	AR089340	AR089340 Sequence	C 476	13.2	14.2	48	6	AX376816	AX376816
C 404	13.2	14.2	28	6	AR093540	AR093540 Sequence	C 477	13.2	14.2	48	6	I20788	I20788
C 405	13.2	14.2	29	6	AX317170	AX317170 Sequence	C 478	13.2	14.2	49	6	AX167831	AX167831
C 406	13.2	14.2	30	6	AR069586	AR069586 Sequence	C 479	13.2	14.2	49	6	AX167832	AX167832
C 407	13.2	14.2	30	6	AR176465	AR176465 Sequence	C 480	13.2	14.2	49	6	AX162484	AX162484
C 408	13.2	14.2	30	6	AX012958	AX012958 Sequence	C 481	13.2	14.2	50	6	MMU041972	MMU041972
C 409	13.2	14.2	31	6	AR08054	AR08054 Synthetic D	C 482	13.2	14.2	50	10	S71710	S71710
C 410	13.2	14.2	31	6	AL3208	AL3208 Oligonucleo	C 483	13.2	14.2	18	9	AX10320	AX10320
C 411	13.2	14.2	31	6	AR034000	AR034000 Sequence	C 484	13.2	14.2	20	6	AX469951	AX469951
C 412	13.2	14.2	31	6	AR124009	AR124009 Sequence	C 485	13.2	14.2	21	6	E06924	E06924
C 413	13.2	14.2	31	6	AR205844	AR205844 Sequence	C 486	13.2	14.2	21	6	AR174640	AR174640
C 414	13.2	14.2	31	6	AX248896	AX248896 Sequence	C 487	13.2	14.2	23	6	AX189414	AX189414
C 415	13.2	14.2	31	6	AX350230	AX350230 Sequence	C 488	13.2	14.2	23	6	AX487373	AX487373
C 416	13.2	14.2	31	6	AX391696	AX391696 Sequence	C 489	13.2	14.2	25	6	E02990	E02990
C 417	13.2	14.2	31	6	AR052657	AR052657 Sequence	C 490	13.2	14.2	25	6	I19377	I19377
C 418	13.2	14.2	33	6	AR103474	AR103474 Sequence	C 491	13.2	14.2	24	11	DOGC004121	DOGC004121
C 419	13.2	14.2	33	6	AR107211	AR107211 Sequence	C 492	13.2	14.2	25	6	AR030291	AR030291
C 420	13.2	14.2	33	6	AR142170	AR142170 Sequence	C 493	13.2	14.2	25	6	AX115968	AX115968
C 421	13.2	14.2	33	6	AR142170	AR142170 Sequence	C 494	13.2	14.2	25	6	AX197046	AX197046
C 422	13.2	14.2	33	6	AR142170	AR142170 Sequence	C 495	13.2	14.2	25	6	AX487373	AX487373
C 423	13.2	14.2	33	6	AR142170	AR142170 Sequence	C 496	13.2	14.2	25	6	E02990	E02990
C 424	13.2	14.2	33	6	AR142170	AR142170 Sequence	C 497	13.2	14.2	25	6	I19377	I19377
C 425	13.2	14.2	33	6	AR142170	AR142170 Sequence	C 498	13.2	14.2	25	6	I19377	I19377
C 426	13.2	14.2	34	6	AR142170	AR142170 Sequence	C 499	13.2	14.2	25	6	I19377	I19377
C 427	13.2	14.2	35	6	AR142170	AR142170 Sequence	C 500	13.2	14.2	26	6	I19377	I19377
C 428	13.2	14.2	35	6	AR142170	AR142170 Sequence	C 501	13.2	14.2	26	6	I19377	I19377
C 429	13.2	14.2	35	6	AR142170	AR142170 Sequence	C 502	13.2	14.2	26	6	I19377	I19377
C 430	13.2	14.2	35	6	AR142170	AR142170 Sequence	C 503	13.2	14.2	26	6	AX419075	AX419075

C 504	13	14.0	27	6	AX117112	AX117112 Sequence	C 577	13	14.0	40	9	HS74585	Z74585 H.sapiens j
C 505	13	14.0	28	6	AR140029	AR140029 Sequence	C 578	13	14.0	41	6	AX076218	AX076218 Sequence
C 506	13	14.0	29	6	AR050496	AR050496 Sequence	C 579	13	14.0	41	6	AX100928	AX100928 Sequence
C 507	13	14.0	29	6	AR124624	AR124624 Sequence	C 580	13	14.0	41	9	HS016757	U16757 Human compl
C 508	13	14.0	29	6	AR201217	AR201217 Sequence	C 581	13	14.0	42	6	AX244233	AX244233 Sequence
C 509	13	14.0	29	6	E44009	E44009 Novel prote	C 582	13	14.0	43	6	AR080524	AR080524 Sequence
C 510	13	14.0	30	6	A11500	A11500 Nucleotide	C 583	13	14.0	43	6	BD010776	BD010776 Specific
C 511	13	14.0	30	6	A46352	A46352 Sequence 3	C 584	13	14.0	44	6	A35023	A35023 Synthetic P
C 512	13	14.0	30	6	A97162	A97162 Sequence 8	C 585	13	14.0	44	6	AR033897	AR033897 Sequence
C 513	13	14.0	30	6	AX364711	AX364711 Sequence	C 586	13	14.0	44	6	AR175030	AR175030 Sequence
C 514	13	14.0	30	6	I45986	I45986 Sequence 10	C 587	13	14.0	45	6	AX032462	AX032462 Sequence
C 515	13	14.0	31	6	AR090018	AR090018 Sequence	C 588	13	14.0	45	6	AR003526	AR003526 Sequence
C 516	13	14.0	31	6	AR121445	AR121445 Sequence	C 589	13	14.0	45	6	BD007254	BD007254 Novel flt
C 517	13	14.0	31	6	AR197053	AR197053 Sequence	C 590	13	14.0	45	6	E37994	E37994 Processes for
C 518	13	14.0	31	6	AX249168	AX249168 Sequence	C 591	13	14.0	45	6	I09496	I09496 Sequence 14
C 519	13	14.0	31	6	AX249248	AX249248 Sequence	C 592	13	14.0	45	6	I28270	I28270 Sequence 5
C 520	13	14.0	31	6	I12138	I12138 Sequence 43	C 593	13	14.0	45	6	I55639	I55639 Sequence 3
C 521	13	14.0	31	6	I41308	I41308 Sequence 43	C 594	13	14.0	47	6	AR4021	AR4021 Sequence 8
C 522	13	14.0	31	6	I49782	I49782 Sequence 5	C 595	13	14.0	47	6	AR079715	AR079715 Sequence
C 523	13	14.0	31	6	I56037	I56037 Sequence 18	C 596	13	14.0	48	6	AR081245	AR081245 Sequence
C 524	13	14.0	31	6	I95908	I95908 Sequence 18	C 597	13	14.0	48	6	AR096588	AR096588 Sequence
C 525	13	14.0	32	6	A67211	A67211 Sequence 2	C 598	13	14.0	48	6	AR105964	AR105964 Sequence
C 526	13	14.0	32	6	AR207932	AR207932 Sequence	C 599	13	14.0	48	6	AR170605	AR170605 Sequence
C 527	13	14.0	32	6	AX034591	AX034591 Sequence	C 600	13	14.0	48	6	AR207730	AR207730 Sequence
C 528	13	14.0	33	6	AR147749	AR147749 Sequence	C 601	13	14.0	48	6	AX274508	AX274508 Sequence
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C 531	13	14.0	33	6	AR169961	AR169961 Sequence	C 604	13	14.0	48	6	I82422	I82422 Sequence 9
C 532	13	14.0	33	6	AR182324	AR182324 Sequence	C 605	13	14.0	48	9	HS7CRA2J	Z28346 H.sapiens (
C 533	13	14.0	33	6	AR199700	AR199700 Sequence	C 606	13	14.0	48	9	574027	574027 TCR alpha V
C 534	13	14.0	33	6	AR202419	AR202419 Sequence	C 607	13	14.0	48	10	MUSIGHYT	M28950 H.sapiens D
C 535	13	14.0	33	6	AR209869	AR209869 Sequence	C 608	13	14.0	48	17	HSCHG60F6	M22397 Mouse Ig ge
C 536	13	14.0	33	6	AX166486	AX166486 Sequence	C 609	13	14.0	49	6	AX329689	AX329689 Sequence
C 537	13	14.0	33	6	E11726	E11726 Primer for	C 610	13	14.0	49	6	AX352745	AX352745 Sequence
C 538	13	14.0	33	6	I65805	I65805 Sequence 13	C 611	13	14.0	49	10	MUSIGHZA	M22397 Mouse Ig ge
C 539	13	14.0	34	6	AX148256	AX148256 Sequence 2	C 612	13	14.0	50	6	AR117420	AR117420 Sequence
C 540	13	14.0	34	6	I56874	I56874 Sequence 2	C 613	13	14.0	50	6	AR131419	AR131419 Sequence
C 541	13	14.0	34	6	AR164511	AR164511 Sequence	C 614	13	14.0	50	6	AR148645	AR148645 Sequence
C 542	13	14.0	35	6	AR164523	AR164523 Sequence	C 615	13	14.0	50	6	AR154225	AR154225 Sequence
C 543	13	14.0	35	6	AX021036	AX021036 Sequence	C 616	13	14.0	50	6	AX136690	AX136690 Sequence
C 544	13	14.0	35	6	I89421	I89421 Sequence 22	C 617	13	14.0	50	6	AX158894	AX158894 Sequence
C 545	13	14.0	36	6	AR030956	AR030956 Sequence	C 618	13	14.0	50	6	AX287016	AX287016 Sequence
C 546	13	14.0	36	6	AR100602	AR100602 Sequence	C 619	13	14.0	50	6	I76130	I76130 Sequence 3
C 547	13	14.0	36	6	S80756	S80756 gamma delta	C 620	13	14.0	50	6	AR153250	AR153250 Sequence
C 548	13	14.0	37	6	AR143569	AR143569 Sequence	C 621	12.8	13.8	17	6	AR210988	AR210988 Sequence
C 549	13	14.0	37	6	AR168938	AR168938 Sequence	C 622	12.8	13.8	17	6	AX227528	AX227528 Sequence
C 550	13	14.0	37	6	E64421	E64421 Peptide hav	C 623	12.8	13.8	19	6	AR067275	AR067275 Sequence
C 551	13	14.0	38	6	AR012832	AR012832 Sequence	C 624	12.8	13.8	20	6	AX294578	AX294578 Sequence
C 552	13	14.0	38	6	AR046328	AR046328 Sequence	C 625	12.8	13.8	21	6	AX095311	AX095311 Sequence
C 553	13	14.0	38	6	AR050303	AR050303 Sequence	C 626	12.8	13.8	21	6	AX153974	AX153974 Sequence
C 554	13	14.0	38	6	AR059775	AR059775 Sequence	C 627	12.8	13.8	21	6	AR053548	AR053548 Sequence
C 555	13	14.0	38	6	AX119260	AX119260 Sequence	C 628	12.8	13.8	22	6	AR065875	AR065875 Sequence
C 556	13	14.0	38	6	AX119889	AX119889 Sequence	C 629	12.8	13.8	22	6	AR080357	AR080357 Sequence
C 557	13	14.0	38	6	AX220450	AX220450 Sequence	C 630	12.8	13.8	22	6	AR143365	AR143365 Sequence
C 558	13	14.0	38	6	AX273594	AX273594 Sequence	C 631	12.8	13.8	22	6	AR148312	AR148312 Sequence
C 559	13	14.0	38	6	BD003217	BD003217 Method fo	C 632	12.8	13.8	22	6	AR168934	AR168934 Sequence
C 560	13	14.0	38	6	I53380	I53380 Sequence 11	C 633	12.8	13.8	22	6	I89419	I89419 Sequence 20
C 561	13	14.0	39	6	AR031582	AR031582 Sequence	C 634	12.8	13.8	24	6	AR049558	AR049558 Sequence
C 562	13	14.0	39	6	AR031582	AR031582 Sequence	C 635	12.8	13.8	24	6	AR065763	AR065763 Sequence
C 563	13	14.0	39	6	BD007260	BD007260 Novel flt	C 636	12.8	13.8	24	6	AR116082	AR116082 Sequence
C 564	13	14.0	39	6	E10381	E10381 PCR primer.	C 637	12.8	13.8	24	6	AR171340	AR171340 Sequence
C 565	13	14.0	39	6	AR078036	AR078036 Sequence	C 638	12.8	13.8	24	6	AX195472	AX195472 Sequence
C 566	13	14.0	40	6	AR116937	AR116937 Sequence	C 639	12.8	13.8	24	6	AX292164	AX292164 Sequence
C 567	13	14.0	40	6	AR171555	AR171555 Sequence	C 640	12.8	13.8	24	6	AX445504	AX445504 Sequence
C 568	13	14.0	40	6	AX045467	AX045467 Sequence	C 641	12.8	13.8	24	6	E15481	E15481 cDNA corres
C 569	13	14.0	40	6	AX078129	AX078129 Sequence	C 642	12.8	13.8	25	6	AX133906	AX133906 Sequence
C 570	13	14.0	40	6	AX371340	AX371340 Sequence	C 643	12.8	13.8	25	6	AX181006	AX181006 Sequence
C 571	13	14.0	40	6	AX56323	AX56323 Sequence	C 644	12.8	13.8	25	6	AX277380	AX277380 Sequence
C 572	13	14.0	40	6	AX56428	AX56428 Sequence	C 645	12.8	13.8	26	6	AR090953	AR090953 Sequence
C 573	13	14.0	40	6	BD005574	BD005574 Compositi	C 646	12.8	13.8	26	6	AR197988	AR197988 Sequence
C 574	13	14.0	40	6	BD005575	BD005575 Compositi	C 647	12.8	13.8	26	6	AX443200	AX443200 Sequence
C 575	13	14.0	40	6	I30267	I30267 Sequence 17	C 648	12.8	13.8	27	6	AX023889	AX023889 Sequence

c 650	12.8	13.8	27	6	AX250712	AX250712 Sequence	c 723	12.8	13.8	40	6	AR029234	AR029234 Sequence
c 651	12.8	13.8	27	6	168167	168167 Sequence 18	c 724	12.8	13.8	40	6	AR059134	AR059134 Sequence
c 652	12.8	13.8	29	6	AR002447	AR002447 Sequence	c 725	12.8	13.8	40	6	AR098730	AR098730 Sequence
c 653	12.8	13.8	29	6	AR028499	AR028499 Sequence	c 726	12.8	13.8	40	6	E35689	E35689 Detection a
c 654	12.8	13.8	29	6	AR154270	AR154270 Sequence	c 727	12.8	13.8	41	6	AR002617	AR002617 Sequence
c 655	12.8	13.8	29	6	AX054843	AX054843 Sequence	c 728	12.8	13.8	41	6	AR099667	AR099667 Sequence
c 656	12.8	13.8	29	6	AX135890	AX135890 Sequence	c 729	12.8	13.8	41	6	AR127597	AR127597 Sequence
c 657	12.8	13.8	29	6	E38404	E38404 SC6 POLYEP	c 730	12.8	13.8	41	6	AR148716	AR148716 Sequence
c 658	12.8	13.8	30	6	AR060637	AR060637 Sequence	c 731	12.8	13.8	41	6	AX357439	AX357439 Sequence
c 659	12.8	13.8	30	6	AR070789	AR070789 Sequence	c 732	12.8	13.8	41	6	175266	175266 Sequence 15
c 660	12.8	13.8	31	6	AR7716	AR7716 Sequence 46	c 733	12.8	13.8	41	9	HS274588	HS274588 H.sapiens J
c 661	12.8	13.8	31	6	AR120447	AR120447 Sequence	c 734	12.8	13.8	42	6	AR154186	AR154186 Sequence
c 662	12.8	13.8	31	6	AR162982	AR162982 Sequence	c 735	12.8	13.8	42	6	AR175513	AR175513 Sequence
c 663	12.8	13.8	31	6	AX201170	AX201170 Sequence	c 736	12.8	13.8	42	6	AR179288	AR179288 Sequence
c 664	12.8	13.8	31	6	AX248097	AX248097 Sequence	c 737	12.8	13.8	42	6	AX201014	AX201014 Sequence
c 665	12.8	13.8	31	6	AX248412	AX248412 Sequence	c 738	12.8	13.8	42	6	AX267813	AX267813 Sequence
c 666	12.8	13.8	31	6	AX248790	AX248790 Sequence	c 739	12.8	13.8	43	6	A20724	A20724 Oligonucleo
c 667	12.8	13.8	31	6	AX249295	AX249295 Sequence	c 740	12.8	13.8	43	6	AR079783	AR079783 Sequence
c 668	12.8	13.8	31	6	AX249705	AX249705 Sequence	c 741	12.8	13.8	43	6	AR081313	AR081313 Sequence
c 669	12.8	13.8	32	6	AR112412	AR112412 Sequence	c 742	12.8	13.8	43	6	AR170673	AR170673 Sequence
c 670	12.8	13.8	33	6	A24333	A24333 Oligonucleo	c 743	12.8	13.8	43	6	AR483530	AR483530 Sequence
c 671	12.8	13.8	33	6	A36954	A36954 Sequence 5	c 744	12.8	13.8	43	9	HS1A533	HS1A533 H.sapiens D
c 672	12.8	13.8	33	6	A39162	A39162 Sequence 10	c 745	12.8	13.8	44	6	AR127634	AR127634 Sequence
c 673	12.8	13.8	33	6	A39221	A39221 Sequence 5	c 746	12.8	13.8	44	6	AX223978	AX223978 Sequence
c 674	12.8	13.8	33	6	AR004375	AR004375 Sequence	c 747	12.8	13.8	44	6	175303	175303 Sequence 52
c 675	12.8	13.8	33	6	AR044765	AR044765 Sequence	c 748	12.8	13.8	45	6	A41693	A41693 Sequence 20
c 676	12.8	13.8	33	6	AR052412	AR052412 Sequence	c 749	12.8	13.8	45	6	AR4819	AR4819 Sequence 14
c 677	12.8	13.8	33	6	AR055210	AR055210 Sequence	c 750	12.8	13.8	45	6	AX137081	AX137081 Sequence
c 678	12.8	13.8	33	6	AR066338	AR066338 Sequence	c 751	12.8	13.8	45	6	AX201013	AX201013 Sequence
c 679	12.8	13.8	33	6	AR073492	AR073492 Sequence	c 752	12.8	13.8	45	6	AX267812	AX267812 Sequence
c 680	12.8	13.8	33	6	AR075497	AR075497 Sequence	c 753	12.8	13.8	45	6	AX455664	AX455664 Sequence
c 681	12.8	13.8	33	6	AR075503	AR075503 Sequence	c 754	12.8	13.8	45	6	AX455665	AX455665 Sequence
c 682	12.8	13.8	33	6	AR077714	AR077714 Sequence	c 755	12.8	13.8	45	9	HUMTCDGC	M28788 Human T-cel
c 683	12.8	13.8	33	6	AR096554	AR096554 Sequence	c 756	12.8	13.8	45	9	568033	568033 Ca(2+)-sens
c 684	12.8	13.8	33	6	AR097166	AR097166 Sequence	c 757	12.8	13.8	46	6	A98787	A98787 Sequence 20
c 685	12.8	13.8	33	6	AR130664	AR130664 Sequence	c 758	12.8	13.8	46	6	AR119840	AR119840 Sequence
c 686	12.8	13.8	33	6	AR157663	AR157663 Sequence	c 759	12.8	13.8	46	6	AX403352	AX403352 Sequence
c 687	12.8	13.8	33	6	AR158081	AR158081 Sequence	c 760	12.8	13.8	46	6	BD007255	BD007255 Novel flt
c 688	12.8	13.8	33	6	AR172013	AR172013 Sequence	c 761	12.8	13.8	47	6	AR119451	AR119451 Sequence
c 689	12.8	13.8	33	6	AR211489	AR211489 Sequence	c 762	12.8	13.8	47	6	AX055775	AX055775 Sequence
c 690	12.8	13.8	33	6	AR211494	AR211494 Sequence	c 763	12.8	13.8	47	6	AX147932	AX147932 Sequence
c 691	12.8	13.8	33	6	AR211500	AR211500 Sequence	c 764	12.8	13.8	47	6	AX194374	AX194374 Sequence
c 692	12.8	13.8	33	6	AX449051	AX449051 Sequence	c 765	12.8	13.8	47	6	AX195005	AX195005 Sequence
c 693	12.8	13.8	33	6	182850	182850 Sequence 29	c 766	12.8	13.8	47	6	AX195065	AX195065 Sequence
c 694	12.8	13.8	33	6	192561	192561 Sequence 87	c 767	12.8	13.8	47	6	AX378296	AX378296 Sequence
c 695	12.8	13.8	34	6	AX024183	AX024183 Sequence	c 768	12.8	13.8	47	6	AX391332	AX391332 Sequence
c 696	12.8	13.8	35	6	AR061924	AR061924 Sequence	c 769	12.8	13.8	48	6	AR032604	AR032604 Sequence
c 697	12.8	13.8	35	6	AX441348	AX441348 Sequence	c 770	12.8	13.8	48	6	AR209268	AR209268 Sequence
c 698	12.8	13.8	35	6	E06670	E06670 DNA probe t	c 771	12.8	13.8	48	6	AX147903	AX147903 Sequence
c 699	12.8	13.8	35	6	125591	125591 Sequence 12	c 772	12.8	13.8	48	6	AX421426	AX421426 Sequence
c 700	12.8	13.8	35	6	125619	125619 Sequence 40	c 773	12.8	13.8	48	6	129344	129344 Sequence 21
c 701	12.8	13.8	35	6	125631	125631 Sequence 52	c 774	12.8	13.8	48	6	191018	191018 Sequence 21
c 702	12.8	13.8	36	6	A39580	A39580 Sequence 19	c 775	12.8	13.8	48	10	MUSIGHYR	M23388 Mouse Ig ge
c 703	12.8	13.8	36	6	A93167	A93167 Sequence 19	c 776	12.8	13.8	48	10	MUSIGHYR	M23388 Mouse Ig ge
c 704	12.8	13.8	36	6	AR071865	AR071865 Sequence	c 777	12.8	13.8	48	10	MD15AB4	MD15AB4 H.domesticu
c 705	12.8	13.8	36	6	AR082501	AR082501 Sequence	c 778	12.8	13.8	49	6	AR007525	AR007525 Sequence
c 706	12.8	13.8	36	6	AR112605	AR112605 Sequence	c 779	12.8	13.8	49	6	AR084091	AR084091 Sequence
c 707	12.8	13.8	36	6	AR166180	AR166180 Sequence	c 780	12.8	13.8	49	6	AX282185	AX282185 Sequence
c 708	12.8	13.8	36	6	AX300777	AX300777 Sequence	c 781	12.8	13.8	49	6	AX282294	AX282294 Sequence
c 709	12.8	13.8	36	6	128161	128161 Sequence 4	c 782	12.8	13.8	49	6	AX322945	AX322945 Sequence
c 710	12.8	13.8	37	6	105907	105907 Sequence 23	c 783	12.8	13.8	49	10	MUSIGHYR	M23395 Mouse Ig ge
c 711	12.8	13.8	37	6	105952	105952 Sequence 23	c 784	12.8	13.8	50	6	AR091559	AR091559 Sequence
c 712	12.8	13.8	37	6	108806	108806 Sequence 6	c 785	12.8	13.8	50	6	AX019326	AX019326 Sequence
c 713	12.8	13.8	37	6	109186	109186 Sequence 24	c 786	12.8	13.8	50	6	AX019327	AX019327 Sequence
c 714	12.8	13.8	38	6	AR004624	AR004624 Sequence	c 787	12.8	13.8	50	6	AX159152	AX159152 Sequence
c 715	12.8	13.8	39	4	S47738	S47738 BOLA-MHC c1	c 788	12.8	13.8	50	6	AX159154	AX159154 Sequence
c 716	12.8	13.8	39	6	AR036762	AR036762 Sequence	c 789	12.8	13.8	50	6	AX159834	AX159834 Sequence
c 717	12.8	13.8	39	6	AR077390	AR077390 Sequence	c 790	12.8	13.8	50	6	AX159836	AX159836 Sequence
c 718	12.8	13.8	39	6	AR077491	AR077491 Sequence	c 791	12.8	13.8	50	6	AX161746	AX161746 Sequence
c 719	12.8	13.8	39	6	AR118010	AR118010 Sequence	c 792	12.8	13.8	50	6	AX165060	AX165060 Sequence
c 720	12.8	13.8	39	6	AX211587	AX211587 Sequence	c 793	12.8	13.8	50	6	AX485732	AX485732 Sequence
c 721	12.8	13.8	39	6	E15776	E15776 PCR primer	c 794	12.8	13.8	50	9	HPBOMINI	K01659 Hepatitis B
c 722	12.8	13.8	39	6	195731	195731 Sequence 59	c 795	12.8	13.8	50	10	AF071601	AF071601 Mus muscu

c 796	12.8	13.8	50	10	F246197810	AP246206 Ratrus no	869	12.6	13.5	30	6	185836	185836 Sequence 4
797	12.8	13.8	50	10	M041979	U41979 Mus musculus	c 870	12.6	13.5	30	23	BD004232	BD004232 Liver fun
798	12.6	13.5	19	6	A39727	A39727 Sequence 1	c 871	12.6	13.5	30	23	BD004249	BD004249 Liver fun
799	12.6	13.5	19	6	AX131251	AX131251 Sequence	872	12.6	13.5	31	6	AX429744	AX429744 Sequence
800	12.6	13.5	20	6	AR031043	AR031043 Sequence	873	12.6	13.5	31	6	143318	143318 Sequence 13
c 801	12.6	13.5	20	6	AR123157	AR123157 Sequence	c 874	12.6	13.5	32	6	A57887	A57887 Sequence 10
802	12.6	13.5	20	6	AR135657	AR135657 Sequence	875	12.6	13.5	32	6	A57148	A57148 Sequence 4
803	12.6	13.5	20	6	AR139527	AR139527 Sequence	c 876	12.6	13.5	32	6	A65154	A65154 Sequence 7
c 804	12.6	13.5	20	6	AR145109	AR145109 Sequence	c 877	12.6	13.5	32	6	A65154	A65154 Sequence 10
c 805	12.6	13.5	20	6	AR160348	AR160348 Sequence	c 878	12.6	13.5	32	6	A65160	A65160 Sequence 16
806	12.6	13.5	20	6	AR162540	AR162540 Sequence	c 879	12.6	13.5	32	6	A68591	A68591 Sequence 5
c 807	12.6	13.5	20	6	AR175931	AR175931 Sequence	c 880	12.6	13.5	32	6	A79376	A79376 Sequence 5
c 808	12.6	13.5	20	6	AR183678	AR183678 Sequence	881	12.6	13.5	32	6	AX052694	AX052694 Sequence
c 809	12.6	13.5	20	6	AR124337	AR124337 Sequence	c 882	12.6	13.5	32	6	AX441365	AX441365 Sequence
c 810	12.6	13.5	20	6	AX397602	AX397602 Sequence	c 883	12.6	13.5	33	6	AX189777	AX189777 Sequence
c 811	12.6	13.5	20	6	E28760	E28760 Antitumor d	c 884	12.6	13.5	33	6	AX449526	AX449526 Sequence
c 812	12.6	13.5	20	6	E28760	E28760 Antitumor d	c 885	12.6	13.5	33	6	BD013171	BD013171 MCH recep
c 813	12.6	13.5	21	6	E28760	E28760 Antitumor d	c 886	12.6	13.5	33	6	BD006652	BD006652 MCH recep
c 814	12.6	13.5	21	6	AR070456	AR070456 Sequence	c 887	12.6	13.5	33	23	BD006652	BD006652 MCH recep
c 815	12.6	13.5	22	6	A33317	A33317 Synthetic A	c 888	12.6	13.5	34	6	AR071831	AR071831 Sequence
c 816	12.6	13.5	22	6	AR067021	AR067021 Sequence	c 889	12.6	13.5	34	6	AR112571	AR112571 Sequence
c 817	12.6	13.5	22	6	AR071087	AR071087 Sequence	c 890	12.6	13.5	34	6	AR137951	AR137951 Sequence
c 818	12.6	13.5	22	6	AR084381	AR084381 Sequence	c 891	12.6	13.5	34	11	C75780	C75780 Homo sapien
c 819	12.6	13.5	22	6	AR135578	AR135578 Sequence	c 892	12.6	13.5	35	6	A69029	A69029 Sequence 17
c 820	12.6	13.5	22	6	AX274669	AX274669 Sequence	c 893	12.6	13.5	35	6	AR120402	AR120402 Sequence
c 821	12.6	13.5	22	6	AX27023	AX27023 Sequence	c 894	12.6	13.5	35	6	AR193479	AR193479 Sequence
c 822	12.6	13.5	22	6	AX27023	AX27023 Sequence	c 895	12.6	13.5	35	6	AX001438	AX001438 Sequence
c 823	12.6	13.5	24	6	AR131011	AR131011 Sequence	c 896	12.6	13.5	35	6	BD006106	BD006106 Refline po
c 824	12.6	13.5	24	6	AX004558	AX004558 Sequence	c 897	12.6	13.5	35	11	C75908	C75908 Homo sapien
c 825	12.6	13.5	24	6	AX004578	AX004578 Sequence	c 898	12.6	13.5	36	6	AR095673	AR095673 Sequence
c 826	12.6	13.5	24	6	AX036649	AX036649 Sequence	c 899	12.6	13.5	36	6	AR160940	AR160940 Sequence
c 827	12.6	13.5	24	6	BD003676	BD003676 Monoclonal	c 900	12.6	13.5	36	6	AR167904	AR167904 Sequence
c 828	12.6	13.5	24	6	EL13490	EL13490 PCR primer	c 901	12.6	13.5	36	6	AR176466	AR176466 Sequence
c 829	12.6	13.5	24	8	ACE91712	ACE91712 Allium ce	c 902	12.6	13.5	36	6	116111	116111 Sequence 18
c 830	12.6	13.5	25	6	A30573	A30573 Synthetic m	c 903	12.6	13.5	36	6	178029	178029 Sequence 73
c 831	12.6	13.5	25	6	AX076238	AX076238 Sequence	c 904	12.6	13.5	37	6	AR009865	AR009865 Sequence
c 832	12.6	13.5	25	6	AX076239	AX076239 Sequence	c 905	12.6	13.5	37	6	AX068536	AX068536 Sequence
c 833	12.6	13.5	26	6	AX365345	AX365345 Sequence	c 906	12.6	13.5	37	6	E00060	E00060 DNA coding
c 834	12.6	13.5	26	6	AX137201	AX137201 Sequence	c 907	12.6	13.5	38	6	AR003429	AR003429 Sequence
c 835	12.6	13.5	27	6	AX137202	AX137202 Sequence	c 908	12.6	13.5	38	6	AR031327	AR031327 Sequence
c 836	12.6	13.5	27	6	AX15337	AX15337 Oligonucleo	c 909	12.6	13.5	38	6	AX201778	AX201778 Sequence
c 837	12.6	13.5	27	6	AX049237	AX049237 Sequence	c 910	12.6	13.5	38	6	AX218764	AX218764 Sequence
c 838	12.6	13.5	27	6	AX049842	AX049842 Sequence	c 911	12.6	13.5	38	6	AX219523	AX219523 Sequence
c 839	12.6	13.5	27	6	AX050840	AX050840 Sequence	c 912	12.6	13.5	38	6	AX222498	AX222498 Sequence
c 840	12.6	13.5	27	6	AX050840	AX050840 Sequence	c 913	12.6	13.5	38	6	AX222507	AX222507 Sequence
c 841	12.6	13.5	28	6	AR038339	AR038339 Sequence	c 914	12.6	13.5	38	6	AX228093	AX228093 Sequence
c 842	12.6	13.5	29	6	EL13597	EL13597 Primer 4/1	c 915	12.6	13.5	38	6	121218	121218 Sequence 64
c 843	12.6	13.5	29	6	AR088677	AR088677 Sequence	c 916	12.6	13.5	38	6	174485	174485 Sequence 64
c 844	12.6	13.5	29	6	AR146958	AR146958 Sequence	c 917	12.6	13.5	39	6	A04101	A04101 Synthetic p
c 845	12.6	13.5	29	6	AR177296	AR177296 Sequence	c 918	12.6	13.5	39	6	AR005203	AR005203 Sequence
c 846	12.6	13.5	29	6	AX099561	AX099561 Sequence	c 919	12.6	13.5	39	6	AR020689	AR020689 Sequence
c 847	12.6	13.5	29	6	AX137243	AX137243 Sequence	c 920	12.6	13.5	39	6	AR061498	AR061498 Sequence
c 848	12.6	13.5	29	6	AX17244	AX17244 Sequence	c 921	12.6	13.5	39	6	AR108397	AR108397 Sequence
c 849	12.6	13.5	29	6	AX175178	AX175178 Sequence	c 922	12.6	13.5	39	6	AR160281	AR160281 Sequence
c 850	12.6	13.5	29	6	AX472705	AX472705 Sequence	c 923	12.6	13.5	39	6	AX278120	AX278120 Sequence
c 851	12.6	13.5	29	6	BD003158	BD003158 Secretary	c 924	12.6	13.5	39	6	116354	116354 Sequence 18
c 852	12.6	13.5	29	6	E26920	E26920 Mutant secr	c 925	12.6	13.5	39	6	166840	166840 Sequence 18
c 853	12.6	13.5	29	6	180077	180077 Sequence 55	c 926	12.6	13.5	39	6	182136	182136 Sequence 11
c 854	12.6	13.5	30	6	A15107	A15107 Oligonucleo	c 927	12.6	13.5	39	6	182216	182216 Sequence 11
c 855	12.6	13.5	30	6	A28868	A28868 Oligonucleo	c 928	12.6	13.5	39	6	184934	184934 Sequence 18
c 856	12.6	13.5	30	6	AR017551	AR017551 Sequence	c 929	12.6	13.5	40	6	AR072531	AR072531 Sequence
c 857	12.6	13.5	30	6	AR122575	AR122575 Sequence	c 930	12.6	13.5	40	6	AX146997	AX146997 Sequence
c 858	12.6	13.5	30	6	AR125672	AR125672 Sequence	c 931	12.6	13.5	40	6	AX456261	AX456261 Sequence
c 859	12.6	13.5	30	6	AR127442	AR127442 Sequence	c 932	12.6	13.5	40	6	115935	115935 Sequence 36
c 860	12.6	13.5	30	6	AR148901	AR148901 Sequence	c 933	12.6	13.5	40	6	196134	196134 Sequence 36
c 861	12.6	13.5	30	6	AX137213	AX137213 Sequence	c 934	12.6	13.5	41	6	A01533	A01533 Joining reg
c 862	12.6	13.5	30	6	AX137214	AX137214 Sequence	c 935	12.6	13.5	41	6	AR027038	AR027038 Sequence
c 863	12.6	13.5	30	6	AX473990	AX473990 Sequence	c 936	12.6	13.5	41	6	AR027039	AR027039 Sequence
c 864	12.6	13.5	30	6	BD011835	BD011835 Liver fun	c 937	12.6	13.5	41	6	AR030628	AR030628 Sequence
c 865	12.6	13.5	30	6	BD011852	BD011852 Liver fun	c 938	12.6	13.5	41	6	AR030629	AR030629 Sequence
c 866	12.6	13.5	30	6	E02945	E02945 DNA sequenc	c 939	12.6	13.5	41	6	AR109152	AR109152 Sequence
c 867	12.6	13.5	30	6	121729	121729 Sequence 4	c 940	12.6	13.5	41	6	AR109153	AR109153 Sequence
c 868	12.6	13.5	30	6	126108	126108 Sequence 34	c 941	12.6	13.5	41	6	AR168166	AR168166 Sequence
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c 942 12.6 13.5 41 6 AR168167 Sequence
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c 944 12.6 13.5 41 6 AR200818 Sequence
c 945 12.6 13.5 41 6 AX085798 Sequence
c 946 12.6 13.5 41 6 183605 Sequence
c 947 12.6 13.5 41 6 183606 Sequence
c 948 12.6 13.5 41 6 AR011352 Sequence
c 949 12.6 13.5 42 6 AR061012 Sequence
c 950 12.6 13.5 42 6 AR061016 Sequence
c 951 12.6 13.5 42 6 AR141000 Sequence
c 952 12.6 13.5 42 6 AR141002 Sequence
c 953 12.6 13.5 42 6 AR141022 Sequence
c 954 12.6 13.5 42 6 AR154181 Sequence
c 955 12.6 13.5 42 6 AR175508 Sequence
c 956 12.6 13.5 42 6 AR179283 Sequence
c 957 12.6 13.5 42 6 AX018723 Sequence
c 958 12.6 13.5 42 6 AX018726 Sequence
c 959 12.6 13.5 42 6 AX047312 Sequence
c 960 12.6 13.5 42 6 AX107166 Sequence
c 961 12.6 13.5 42 6 AX111385 Sequence
c 962 12.6 13.5 42 6 103611 Sequence
c 963 12.6 13.5 42 6 117990 Sequence
c 964 12.6 13.5 42 6 117990 Sequence
c 965 12.6 13.5 43 5 AP1DBEC
c 966 12.6 13.5 43 5 A79867 Sequence
c 967 12.6 13.5 43 6 AR014640 Sequence
c 968 12.6 13.5 43 6 AR028012 Sequence
c 969 12.6 13.5 43 6 AR028016 Sequence
c 970 12.6 13.5 43 6 AR157604 Sequence
c 971 12.6 13.5 43 6 AX034935 Sequence
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c 973 12.6 13.5 43 6 AX477729 Sequence
c 974 12.6 13.5 44 6 BD010432 Sequence
c 975 12.6 13.5 44 6 AX026707 Sequence
c 976 12.6 13.5 45 6 AX297575 Sequence
c 977 12.6 13.5 45 6 HSEH1B
c 978 12.6 13.5 45 6 HDMGLTASP
c 979 12.6 13.5 46 6 129950 Sequence
c 980 12.6 13.5 46 6 A25667
c 981 12.6 13.5 47 6 AX180261 Sequence
c 982 12.6 13.5 47 6 AX194736 Sequence
c 983 12.6 13.5 47 6 AX195022 Sequence
c 984 12.6 13.5 47 6 AX212303 Sequence
c 985 12.6 13.5 47 6 AX278085 Sequence
c 986 12.6 13.5 47 6 AX378310 Sequence
c 987 12.6 13.5 47 6 AX378363 Sequence
c 988 12.6 13.5 47 6 AX480644 Sequence
c 989 12.6 13.5 47 6 HDMCFINSCA
c 990 12.6 13.5 48 6 AR019025 Sequence
c 991 12.6 13.5 48 6 AR032616 Sequence
c 992 12.6 13.5 48 6 AR071302 Sequence
c 993 12.6 13.5 48 6 AR079463 Sequence
c 994 12.6 13.5 48 6 AR126786 Sequence
c 995 12.6 13.5 48 6 AR130425 Sequence
c 996 12.6 13.5 48 6 AR202443 Sequence
c 997 12.6 13.5 48 6 AR202480 Sequence
c 998 12.6 13.5 48 6 AX322133 Sequence
c 999 12.6 13.5 48 6 AX403498 Sequence
1000 12.6 13.5 48 6 BD011312 Human tel

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ALIGNMENTS

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RESULT 1 45 bp DNA Linear PAT 31-DEC-2000
LOCUS AR078468
DEFINITION Sequence 8 from patent US 5966664.
ACCESSION AR078468
VERSION AR078468.1 GI:10005214
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```

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REFERENCE
AUTHORS 1 (bases 1 to 45)
TITLE Friedhoff,A.J., Basham,D.A. and Miller,J.C.
JOURNAL Psychosis protecting nucleic acid, peptides, compositions and
FEATURES
SOURCE Patent: US 5966664-A 8 05-OCT-1999;
LOCATION/Qualifiers
BASE COUNT 14 a 15 c 8 g 8 t
ORIGIN
Query Match 20.0%; Score 18.6; DB 6; Length 45;
Best Local Similarity 84.0%; Pred. No. 2.7e+04;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 10 GCACGCCATTCCTGCGGTGACAA 34
Db 4 GCACGCCATTCCTGCGGTGACAA 28

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RESULT 2 30 bp DNA Linear PAT 01-DEC-1993
LOCUS A11493
DEFINITION Nucleotide sequence 33 from patent number EP0170204.
ACCESSION A11493
VERSION A11493.1 GI:492477
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hauptmann,R., Meindl,P., Dworkin-Rastl,E., Adolf,G.D., Smetly,P.,
TITLE Piefer,C. and Hanel,N.
JOURNAL Genetic sequences, type I interferon peptide coded by them, and
these organisms producing the same
PATENT: EP 0170204-A 33 05-FEB-1986;
BOEHRINGER INGELHEIM INTERNATIONAL GmbH
FEATURES
SOURCE Location/Qualifiers
1. 30
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 6 c 10 g 8 t
ORIGIN

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Query Match 18.5%; Score 17.2; DB 6; Length 30;
Best Local Similarity 86.4%; Pred. No. 9.2e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 GGAGCAGCTCCATTCGCTGGG 28
Db 9 GGAGCAGCTCCATTCGCTGGG 30

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RESULT 3 49 bp DNA Linear PAT 14-JUN-2002
LOCUS AX404630
DEFINITION Sequence 4 from Patent W00224745.
ACCESSION AX404630
VERSION AX404630.1 GI:21437911
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Abken,H. and Schinkoethe,T.
TITLE Method for detecting tumor cells
JOURNAL Patent: WO 0224745-A 4 28-MAR-2002;
Abken, Hinrich (DE)
FEATURES
SOURCE Location/Qualifiers
1. 49
/organism="Homo sapiens"

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BASE COUNT      12 a      8 c      11 g      18 t
ORIGIN

Query Match
Best Local Similarity 18.3%; Score 17; DB 6; Length 49;
Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 5 TGGGAGCAGCTCCGCTGCGGAGTGTGACATGCTGCTT 45
DB 2 TGGAAACTCCACTCCTTGTTCAGAGTGCGTGGCT 42

RESULT 4
AX159154
LOCUS AX159154 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2482 from Patent WO0140521.
ACCESSION AX159154
VERSION AX159154.1 GI:14540485
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS methods of use thereof
JOURNAL Patent: WO 0140521-A 2482 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1..50
misc-feature /organism="Homo sapiens"
/db_xref="taxon:9606"
25..26
misc_ /note="Nucleotide deleted between bases 25 and 26
Accession number cg39667412"
26
misc-feature /note="2 of 2 allelic variants (2481 is other entry)"
BASE COUNT 13 a 13 c 13 g 11 t
ORIGIN

Query Match
Best Local Similarity 18.1%; Score 16.8; DB 6; Length 50;
Matches 27; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 37 CCTGCTTCAACACTATGAGATGTGCTGCGGCTCCAGA 80
DB 5 CCATGGCGTGCACACAGAGGAGCTGTCATACACAGCTTCATA 48

RESULT 5
AR093240
LOCUS AR093240 30 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 14 from patent US 5998697.
ACCESSION AR093240
VERSION AR093240.1 GI:10019990
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Devlin, R.H.
TITLE Transgenic fish and vectors therefor
JOURNAL Patent: US 5998697-A 14 07-DEC-1999;
FEATURES
source location/Qualifiers
1..30
misc_ /organism="unknown"
BASE COUNT 8 a 8 c 8 g 6 t
ORIGIN

Query Match
Best Local Similarity 17.8%; Score 16.6; DB 6; Length 30;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 43 TTTCACACTATGAGATGTGCTGCGGCT 73
DB 7 ATTCGCTGCTGCTGCTGCTGCTGCT 39
DB 7 ATCCAGCTGATGATGATGATGATGAT 29

RESULT 6
CT5763/c
LOCUS CT5763/c 34 bp DNA linear STS 12-FEB-1999
DEFINITION Homo sapiens STS NIB517, DH PROBE, FORWARD PRIMER, sequence tagged
site.
ACCESSION CT5763
VERSION CT5763.1 GI:3176205
KEYWORDS STS; DH; digital hybridization.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Asakawa, S. and Shimizu, N.
TITLE High-fidelity digital hybridization screening
JOURNAL Genomics 49 (2), 209-217 (1998)
MEDLINE 98260670
REFERENCE 2 (bases 1 to 34)
AUTHORS Asakawa, S. and Shimizu, N.
TITLE Direct Submersion
JOURNAL Submitted (09-SEP-1997) Shuichi Asakawa, Keio University School of
Medicine, Department of Molecular Biology, Shinanomachi 35,
Shinjuku-ku, Tokyo 160, Japan (E-mail: asaedmb.med.keio.ac.jp,
Tel:81-3-3351-2370)
FEATURES
source location/Qualifiers
1..34
misc_ /organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 11 a 8 c 7 g 8 t
ORIGIN

Query Match
Best Local Similarity 17.8%; Score 16.6; DB 11; Length 34;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 TGGGAGCAGCTCCATCTTCCTGCTGACAT 35
DB 31 TGTGAGCTAGTATTCAGCTGCTGTAACAT 1

RESULT 7
I44807/c
LOCUS I44807/c 39 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 31 from patent US 5635599.
ACCESSION I44807
VERSION I44807.1 GI:2469520
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Pastan, I.H., Kreitman, R.J. and Puri, R.K.
TITLE Fusion Proteins comprising circularly permuted ligands
JOURNAL Patent: US 5635599-A 31 03-JUN-1997;
FEATURES
source location/Qualifiers
1..39
misc_ /organism="unknown"
BASE COUNT 7 a 10 c 12 g 10 t
ORIGIN

Query Match
Best Local Similarity 17.8%; Score 16.6; DB 6; Length 39;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 43 TTTCACACTATGAGATGTGCTGCGGCT 73
DB 7 ATTCGCTGCTGCTGCTGCTGCTGCT 39
DB 7 ATCCAGCTGATGATGATGATGATGAT 29

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Db 35 TCTCACACTCACCGAGGTACGCTGGGC 5

RESULT 8

LOCUS 179331 49 bp DNA linear PAT 10-JUN-1998
 DEFINITION Sequence 34 from patent US 5707796.
 VERSION 179331
 KEYWORDS 179331.1 GI:3207621
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 49)
 AUTHORS Gold, L. and Beutel, B.
 TITLE Method for selecting nucleic acids on the basis of structure
 JOURNAL Patent: US 5707796-A 34 13-JAN-1998;
 FEATURES Location/Qualifiers
 source 1..49

BASE COUNT 13 a 12 c 13 g 11 t
 ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 49;
 Best Local Similarity 71.0%; Pred. No. 1.7e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 49 CACTATCGAATGTACTGTGGGCTCCAG 79
 19 CACTATAGGAGATGCTGTGAGCATGCTG 49

RESULT 9
 LOCUS ARI25663 50 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 5 from patent US 6177557.
 ACCESSION ARI25663
 VERSION ARI25663.1 GI:14111725
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
 AUTHORS Janjic, N., Gold, L., and Tasset, D.
 TITLE High affinity ligands of basic fibroblast growth factor and thrombin
 JOURNAL Patent: US 6177557-A 5 23-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..50

BASE COUNT 13 a 13 c 13 g 11 t
 ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 50;
 Best Local Similarity 71.0%; Pred. No. 1.7e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 49 CACTATCGAATGTACTGTGGGCTCCAG 79
 20 CACTATAGGAGATGCTGTGAGCATGCTG 50

RESULT 10

LOCUS 147075 50 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 5 from patent US 5639868.
 ACCESSION 147075
 VERSION 147075.1 GI:2471040
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
 Unclassified.

AUTHORS Janjic, N. and Gold, L.
 TITLE High-affinity RNA ligands for basic fibroblast growth factor
 JOURNAL Patent: US 5639868-A 5 17-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..50

BASE COUNT 13 a 13 c 13 g 11 t
 ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 50;
 Best Local Similarity 71.0%; Pred. No. 1.7e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 49 CACTATCGAATGTACTGTGGGCTCCAG 79
 20 CACTATAGGAGATGCTGTGAGCATGCTG 50

RESULT 11

LOCUS ARI49818 47 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 19 from patent US 6228621.
 ACCESSION ARI49818
 VERSION ARI49818.1 GI:15114409
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 47)
 AUTHORS Williams, W.V., Madato, M., and Weiner, D.B.
 TITLE Plasmids encoding immunogenic proteins and intracellular targeting sequences
 JOURNAL Patent: US 6228621-A 19 08-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..47

BASE COUNT 11 a 12 c 11 g 10 t 3 others
 ORIGIN

Query Match 17.6%; Score 16.4; DB 6; Length 47;
 Best Local Similarity 60.5%; Pred. No. 2.1e+05;
 Matches 23; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Db 55 CGGAATGTACTGTGGGCTCCAGAAACATGAGGT 92
 46 CAGRYGYTGACGCTGTGAGCATGCTGATTAAGATTAGAT 9

RESULT 12

LOCUS BD007169 47 bp DNA linear PAT 31-JAN-2002
 DEFINITION Improved vaccines.
 ACCESSION BD007169
 VERSION BD007169.1 GI:1863540
 KEYWORDS JP 2001503260-A/14.
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 47)
 AUTHORS Williams, W.V., Madato, M., and Weiner, D.B.
 TITLE Improved vaccines
 JOURNAL Patent: JP 2001503260-A 14 13-MAR-2001;
 COMMENT THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
 OS Unknown
 PN JP 2001503260-A/14
 PD 13-MAR-2001
 PE 23-OCT-1997 JP 1998519728
 PR 23-OCT-1996 US 60/029592
 PI WILLIAM V WILLIAMS, MICHAEL MADATO, DAVID B WEHNER PC
 CC C12N15/09, A61K48/00//A61K39/00, C12N15/00

FT Key Location/Qualifiers
 FT source 1..47

FEATURES	FT	Location/Qualifiers	source	1. 47	/organism="unknown".
BASE COUNT	11 a	12 c	11 g	10 t	3 others
ORIGIN					
Query Match	17.6%;	Score 16.4;	DB 6;	Length 47;	
Best Local Similarity	60.5%;	Pred. No. 2.1e+05;			
Matches	23;	Conservative	2;	Mismatches 13;	Indels 0; Gaps 0;
OY	55	CGGATGTGACCTGTGGCCCTCCAGAAAACATTGAGGT	92		
Db	46	CAGRYGTGTGACCTGCAGCCTCGATTAAGATTGAT	9		
RESULT 13					
LOCUS	AX159152	50 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 2480 from Patent WO0140521.				
ACCESSION	AX159152				
VERSION	AX159152.1	GI:14540483			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 50)				
JOURNAL	Shinketsu, R.A. and Leach, M.				
FEATURES	Nucleic acids containing single nucleotide polymorphisms and				
source	Methods of use thereof				
Patent:	WO 0140521-A 2480 07-JUN-2001;				
Curagen Corporation (US)					
Location/Qualifiers					
1. 50					
/organism="Homo sapiens"					
/db_xref="taxon:9606"					
misc-feature	25. 26				
/note="Nucleotide deleted between bases 25 and 26					
Accession number	cg39667412"				
misc-feature	26				
/note="2 of 2 allelic variants (2479 is other entry)"					
BASE COUNT	13 a	15 c	13 g	9 t	
ORIGIN					
Query Match	17.6%;	Score 16.4;	DB 6;	Length 50;	
Best Local Similarity	61.9%;	Pred. No. 2.1e+05;			
Matches	26;	Conservative	0;	Mismatches 16;	Indels 0; Gaps 0;
OY	37	CCTTGTTTCACACTATCGAATGTGATGTCGGGCTCCA	78		
Db	9	CCATGGCGTCACACAGAGGACTGTGCATACACAGCGTTTCA	50		
RESULT 14					
LOCUS	AR078049	40 bp	DNA	linear	PAT 31-AUG-2000
DEFINITION	Sequence 103 from patent US 5962272.				
ACCESSION	AR078049				
VERSION	AR078049.1	GI:10004795			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 40)				
TITLE	Chenichik, A., Zhu, Y., Diatchenko, L. and Siebert, P.				
JOURNAL	Methods and compositions for full-length CDNA Cloning using a				
Patent:	US 5962272-A 103 05-OCT-1999;				
Curagen Corporation (US)					
Location/Qualifiers					
1. 40					
/organism="unknown"					

BASE COUNT	12 a	9 c	16 g	3 t
ORIGIN				
Query Match	17.4%;	Score 16.2;	DB 6;	Length 40;
Best Local Similarity	64.9%;	Pred. No. 2.4e+05;		
Matches	24;	Conservative	0;	Mismatches 13;
OY	3	GCTGGGAGCACTCCATTCCTGCGGTCGACAGCCCT	39	
Db	37	GCTGCTGCTGCCACCTGCTGCTGTACCACTGCTT	1	
RESULT 15				
LOCUS	HSTCR2J	48 bp	mRNA	linear
DEFINITION	H.sapiens (K2.4) T-cell receptor alpha-chain joining region.			
ACCESSION	Z28346			
VERSION	Z28346.1	GI:607118		
KEYWORDS	immunoglobulin alpha-chain; immunoglobulin joining region; T-cell			
SOURCE	receptor alpha-chain joining region.			
ORGANISM	Homo sapiens.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 48)			
JOURNAL	Durbinovic-Bello, I., Steinle, A., Ziegler, A.G. and Schendel, D.J.			
FEATURES	Unpublished			
source	2 (bases 1 to 48)			
Steinle, A.				
Direct Submission				
Submitted (22-NOV-1993)	Steinle A., University of Munich, Institute			
of Immunology, Goethestrasse 31, D-80336 MÜNCHEN, GERMANY				
Location/Qualifiers				
1. 48				
/organism="Homo sapiens"				
/isolate="AS"				
/db_xref="taxon:9606"				
/chromosome="14"				
/clone="K2.4"				
/haplotype="DRB1*0401 DOA1*0301 DOB1*0302"				
/cell_type="CD4+ T-cell clone"				
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/note="T-cell receptor alpha-chain joining region				
(Val.3-N-Ja08)"				
/codon_start=1				
/evidence=experimental				
/product="T-cell receptor alpha-chain joining region"				
/protein_id="CAA82200.1"				
/db_xref="GI:607119"				
/translation="CAVTPGSGGYNKLIF"				

AUTHORS Brown, W.C.
TITLE Highly efficient controlled expression of exogenous genes in e. coli
JOURNAL Patent: US 6180391-A 6 30-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1.40
BASE COUNT 13 a 9 c 10 g 8 t
ORIGIN

Query Match 17.0%; Score 15.8; DB 6; Length 40;
Best Local Similarity 74.1%; Pred. No. 3.5e+05;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 11 CACTCATTCTGCGTGGGACAAATGC 37
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Db 27 CACTCATTCTGCTACTGCTTGCACAAAGC 1

RESULT 20
ARI09086/c ARI09086 42 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 45 from patent US 6114116.
ACCESSION ARI09086
VERSION ARI09086.1 GI:12825362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Lemieux, B., Landry, B.S. and Sapolsky, R.J.
TITLE Brassica polymorphisms
JOURNAL Patent: US 6114116-A 45 05-SEP-2000;
FEATURES Location/Qualifiers
SOURCE 1.42
BASE COUNT 14 a 11 c 11 g 6 t
ORIGIN

Query Match 17.0%; Score 15.8; DB 6; Length 42;
Best Local Similarity 74.1%; Pred. No. 3.5e+05;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 43 TTTCACACTATCGGAATGTGACTGTC 69
||||| ||| ||| ||| ||| ||| |||
Db 32 TTTCGACTCTGTGGGACTGTACTGTC 6

RESULT 21
AR200741/c AR200741 42 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 45 from patent US 6358686.
ACCESSION AR200741
VERSION AR200741.1 GI:20251629
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Lemieux, B., Landry, B.S. and Sapolsky, R.J.
TITLE Brassica polymorphisms
JOURNAL Patent: US 6358686-A 45 19-MAR-2002;
FEATURES Location/Qualifiers
SOURCE 1.42
BASE COUNT 14 a 11 c 11 g 6 t
ORIGIN

Query Match 17.0%; Score 15.8; DB 6; Length 42;
Best Local Similarity 74.1%; Pred. No. 3.5e+05;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 43 TTTCACACTATCGGAATGTGACTGTC 69

Db 32 TTTCGACTCTGTGGGACTGTACTGTC 6
||||| ||| ||| ||| ||| ||| |||

RESULT 22
I43354/c I43354 44 bp DNA linear PAT 07-OCT-1997
LOCUS I43354
DEFINITION Sequence 8 from patent US 5631150.
ACCESSION I43354
VERSION I43354.1 GI:2468598
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Haraki, A.M., Watanabe, A.N., Arai, J.H.A. and Pastinen, O.A.
TITLE Manufacturing of xyliol using recombinant microbial hosts
JOURNAL Patent: US 5631150-A 8 20-MAY-1997;
FEATURES Location/Qualifiers
SOURCE 1.44
BASE COUNT 11 a 8 c 10 g 15 t
ORIGIN

Query Match 17.0%; Score 15.8; DB 6; Length 44;
Best Local Similarity 74.1%; Pred. No. 3.5e+05;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 8 GAGCCTCATCTGCTGCGGTGACAA 34
||||| ||| ||| ||| ||| ||| |||
Db 39 GACCATTCATCTCTAAGGCTGACAA 13

RESULT 23
AX417271 AX417271 27 bp DNA linear PAT 18-JUN-2002
LOCUS AX417271
DEFINITION Sequence 16 from Patent WO0230978.
ACCESSION AX417271
VERSION AX417271.1 GI:21522581
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Murphy, A.J.
TITLE Polypeptides, methods of making, and uses thereof
JOURNAL Patent: WO 0230978-A 16 18-APR-2002;
REGENERON PHARMA (US)
FEATURES Location/Qualifiers
SOURCE 1.27
BASE COUNT 9 a 7 c 7 g 4 t
ORIGIN

Query Match 16.8%; Score 15.6; DB 6; Length 27;
Best Local Similarity 81.8%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGCTGGAGAGCACTCCATTCTG 22
||||| ||| ||| ||| ||| ||| |||
Db 2 GACCTGGAGAGAACCACTCTG 23

RESULT 24
AR022050 AR022050 33 bp DNA linear PAT 05-DEC-1998
LOCUS AR022050
DEFINITION Sequence 14 from patent US 5792456.
ACCESSION AR022050
VERSION AR022050.1 GI:3976112
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Yelton,D., Glaser,S., Huse,W. and Rosok,M.Joanne.
TITLE Mutant BR96 antibodies reactive with human carcinomas
JOURNAL Patent: US 5792456-A 14 11-AUG-1998;
FEATURES Location/Qualifiers
source 1..33
BASE COUNT 12 a 7 c 7 g 7 t
ORIGIN
Query Match 16.8%; Score 15.6; DB 6; Length 33;
Best Local Similarity 81.8%; Pred. No. 4e+05;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 70 GGGCTTCAGAAAACATTGAGG 91
Db 2 GGGACTTCAGAAAAGCTTTAGG 23
RESULT 25
LOCUS 192840 33 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 14 from patent US 5728821.
ACCESSION 192840
VERSION 192840.1 GI:3937310
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Yelton,D., Glaser,S., Huse,W. and Rosok,M.Joanne.
TITLE Mutant BR96 antibodies reactive with human carcinomas
JOURNAL Patent: US 5728821-A 14 17-MAR-1998;
FEATURES Location/Qualifiers
source 1..33
BASE COUNT 12 a 7 c 7 g 7 t
ORIGIN
Query Match 16.8%; Score 15.6; DB 6; Length 33;
Best Local Similarity 81.8%; Pred. No. 4e+05;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 70 GGGCTTCAGAAAACATTGAGG 91
Db 2 GGGACTTCAGAAAAGCTTTAGG 23
RESULT 26
E27408 35 bp DNA linear PAT 18-JUN-2001
LOCUS
DEFINITION Process for producing organic acid by pyruvate carboxylase gene
recombinant.
ACCESSION E27408.1 GI:13018213
VERSION JP 1999196888-A/10.
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Takashi,K., Makoto,G., Masato,T. and Hideaki,Y.
TITLE Process for producing organic acid by pyruvate carboxylase gene
recombinant
JOURNAL Patent: JP 1999196888-A 10 27-JUL-1999;
MITSUBISHI CHEM CORP
OS unidentified
PN JP 1999196888-A/10
PD 27-JUL-1999
PF 16-JAN-1998 JP 1998020361
PI TAKASHI KOBAYASHI, MAKOTO GOTO, MASATO TERASAWA, HIDEAKI YUKAWA

PC C12P7/40,C12N1/21,C12N15/09//C12P7/40,C12R1.13), (C12N1/21, PC
C12R1.13),
PC (C12N15/09,C12R1.865),C12N15/00,(C12N15/00,C12R1.865) CC
Strandedness: Single;
CC Topology: linear;
FH Key Location/Qualifiers
FT source 1..35
FT /organism='unidentified'.
FEATURES
source 1..35
Location/Qualifiers
/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 8 a 9 c 7 g 11 t
ORIGIN
Query Match 16.8%; Score 15.6; DB 6; Length 35;
Best Local Similarity 81.8%; Pred. No. 4.1e+05;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 34 ATGCTTGGTTCAACACTATC 55
Db 14 ATGCTTGGTTCAACAGAAC 35
RESULT 27
F202550S09 43 bp DNA linear PRI 02-AUG-2000
LOCUS Homo sapiens DNA methyltransferase (DNMT1) gene, intron 9.
DEFINITION AF202558
ACCESSION AF202558.1 GI:9651502
VERSION
KEYWORDS
SEGMENT
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 43)
AUTHORS Ramchandani,S., Bigey,P. and Szyf,M.
TITLE Genomic structure of the human DNA methyltransferase gene
JOURNAL Biol. Chem. 379 (4-5), 535-540 (1998)
MEDLINE 98290312
PUBMED 9628348
REFERENCE 2 (bases 1 to 43)
AUTHORS Ramchandani,S., Bigey,P. and Szyf,M.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1999) Pharmacology and Therapeutics, McGill
University, 3655 Promenade Sir William Osler, Montreal, Quebec
H3G-1Y6, Canada
FEATURES
source 1..43
Location/Qualifiers
/organism='Homo sapiens'
/db_xref='taxon:9606'
misc_feature 1..43
/gene='DNMT1'
/note='contains intron 9'
BASE COUNT 2 a 6 c 13 g 22 t
ORIGIN
Query Match 16.8%; Score 15.6; DB 9; Length 43;
Best Local Similarity 70.0%; Pred. No. 4.2e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 18 TTCTGCTGGGTGACAAATGCTTGGTTCA 47
Db 8 TTCTGTTGGGTGTTGGTCTTGGTTGA 37
RESULT 28
AX457962/C 44 bp DNA linear PAT 08-JUL-2002
LOCUS AX457962
DEFINITION Sequence 4 from Patent WO0246456.
ACCESSION AX457962.1 GI:21724857
VERSION

ACCESSION AR051493
VERSION AR051493.1 GI:5974857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 31)
TITLE de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 63 03-NOV-1998;
FEATURES Location/Qualifiers
SOURCE 1..31
BASE COUNT 6 a 10 c 8 g 7 t
ORIGIN
Query Match 16.3%; Score 15.2; DB 6; Length 31;
Best Local Similarity 85.0%; Pred. No. 5.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTCAGCCTGGGTGACAGAC 8
RESULT 37
LOCUS AR072633 31 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 63 from patent US 5948634.
ACCESSION AR072633
VERSION AR072633.1 GI:9999397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 31)
TITLE de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948634-A 63 07-SEP-1999;
FEATURES Location/Qualifiers
SOURCE 1..31
BASE COUNT 6 a 10 c 8 g 7 t
ORIGIN
Query Match 16.3%; Score 15.2; DB 6; Length 31;
Best Local Similarity 85.0%; Pred. No. 5.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTCAGCCTGGGTGACAGAC 8
RESULT 38
LOCUS AR073178 31 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 63 from patent US 5948888.
ACCESSION AR073178
VERSION AR073178.1 GI:9999941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 31)
TITLE de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948888-A 63 07-SEP-1999;
FEATURES Location/Qualifiers
SOURCE 1..31

BASE COUNT 6 a 10 c 8 g 7 t
ORIGIN
Query Match 16.3%; Score 15.2; DB 6; Length 31;
Best Local Similarity 85.0%; Pred. No. 5.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTCAGCCTGGGTGACAGAC 8
RESULT 39
LOCUS AX248615 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 694 from Patent WO0166800.
ACCESSION AX248615
VERSION AX248615.1 GI:15863238
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 016800-A 694 13-SEP-2001;
FEATURES WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
SOURCE 1..31
BASE COUNT 6 a 6 c 13 g 5 t 1 others
ORIGIN
Query Match 16.3%; Score 15.2; DB 6; Length 31;
Best Local Similarity 77.3%; Pred. No. 5.8e+05;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 15 CCATTGCGCTGGGTGACATGC 36
DB 22 CCGCTGCGCTGGGTGACATGC 1
RESULT 40
LOCUS AX468447 15 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 15 from Patent WO0216594.
ACCESSION AX468447
VERSION AX468447.1 GI:21901283
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Chesnut,J.D., Shuman,S., Madden,K.R., Heyman,J. and Bennett,R.P.
TITLE Methods and reagents for molecular cloning
JOURNAL Patent: WO 0216594-A 15 28-FEB-2002;
INITIATOR INTRON CORPORATION (US); Sloan-Kettering Institute For Cancer Research (US)
FEATURES Location/Qualifiers
SOURCE 1..15
BASE COUNT 6 a 4 c 2 g 3 t
ORIGIN
Query Match 16.1%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAACACTATCGAAT 60
Db 1 CAACACTATCGAAT 15

RESULT 41
LOCUS 116731 25 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 8 from patent US 5476926.
ACCESSION 116731
VERSION 116731.1 GI:1251639
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Spiegelman, B.M., Graves, R. and Ross, S.
TITLE Adipocyte-specific DNA sequences and use thereof in the production of transgenic animals exhibiting altered fat tissue metabolism
JOURNAL Patent: US 5476926-A 8 19-DEC-1995;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"

BASE COUNT 9 a 4 c 7 g 5 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 25;
Best Local Similarity 78.3%; Pred. No. 6.7e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 CACTCCATCTGCTGGGTGACA 33
Db 24 CAATCCCTCTCTCTGGGTGAAA 2

RESULT 42
AX249653/c 31 bp DNA linear PAT 28-SEP-2001
LOCUS AX249653
DEFINITION Sequence 1732 from Patent WO0166800.
ACCESSION AX249653
VERSION AX249653.1 GI:15864276
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 31)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Cargill, M., Ireland, J.S. and Lander, E.S.
JOURNAL Human single nucleotide polymorphisms
Patent: WO 0166800-A 1732 13-SEP-2001;
FEATURES Location/Qualifiers
source 1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 8 a 10 c 7 g 5 t 1 others
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 31;
Best Local Similarity 72.0%; Pred. No. 6.9e+05;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 28 GTGACATGCTGCTGTTCAACACT 52
Db 28 GTGATGTCCTGCTGCTGTTCAACT 4

RESULT 43
AR085045/c 32 bp DNA linear PAT 01-SEP-2000
LOCUS AR085045
DEFINITION Sequence 7 from patent US 5981262.
ACCESSION AR085045
VERSION AR085045.1 GI:10011816

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Brugge, J., Morganstern, J., Shue, L., Zydowsky, L., Zoller, M. and Pawson, A.
TITLE Human syk
JOURNAL Patent: US 5981262-A 7 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"

BASE COUNT 6 a 11 c 4 g 7 t 4 others
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 32;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 28 GTGACATGCTGCTGTTCA 47
Db 32 GAGAAATGCTGCTGTTCA 13

RESULT 44
116735/c 33 bp DNA linear PAT 03-APR-1996
LOCUS 116735
DEFINITION Sequence 12 from patent US 5476926.
ACCESSION 116735
VERSION 116735.1 GI:1251643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Spiegelman, B.M., Graves, R. and Ross, S.
TITLE Adipocyte-specific DNA sequences and use thereof in the production of transgenic animals exhibiting altered fat tissue metabolism
JOURNAL Patent: US 5476926-A 12 19-DEC-1995;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 9 a 8 c 10 g 6 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 7e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 CACTCCATCTGCTGGGTGACA 33
Db 33 CAATCCCTCTCTCTGGGTGAAA 11

RESULT 45
AR127205/c 36 bp DNA linear PAT 16-MAY-2001
LOCUS AR127205
DEFINITION Sequence 9 from patent US 6180391.
ACCESSION AR127205
VERSION AR127205.1 GI:14113798
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Brown, W.C.
TITLE Highly efficient controlled expression of exogenous genes in e. coli
JOURNAL Patent: US 6180391-A 9 30-JAN-2001;
FEATURES Location/Qualifiers
source 1..36
/organism="unknown"

BASE COUNT 8 a 8 c 8 g 12 t

ORIGIN

Query Match	16.1%;	Score 15;	DB 6;	Length 36;
Best Local Similarity	78.3%;	Pred. NO. 7.1e+05;		
Matches 18;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

```

OY      1 GAGCTGGGAGCACTCCATTCTGC 23
          ||| ||| | | ||||| 7|
Db      35 GAGTTGGAGGAATCCATTCAGC 13

```

RESULT 46
ARI127206
11-2001
DATE 10 NOV 2001
36 L-
0000000000

Query Match	16.1%;	Score 15;	DB 6;	Length 36;
Best Local Similarity	78.3%;	Pred. No. 7.1e+05;		
Matches 18;	Conservative	0;	Mismatches 5;	Indels 0;

QY	1	GAGCTGGGAGCACTCCATTTCTGC	23
Db	8	GAGTTGAAGAATTCATTCAGC	30

RESULT 47			
AR019012/c			
LOCUS	AR019012	41 bp	DNA
DEFINITION	Sequence 91 from patent US 5783195.		linear
			PAT 05-DEC-1996

Query Match	16.18;	Score 15;	DB 6;	Length 41;
Best Local Similarity	67.78;	Pred. No. 7.2e+05;		
Matches 21; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

```

OY      33 AATGCCCTGGTTTCACACTATCGGAATGTC 63
        ||| ||| | | | | | | | |
Db      40 AATGCTTGAATTTAAGATGATGGGTATGAG 100

```

RESULT 48
AR111609/c

LOCUS	AR111609	41 bp	DNA	linear	PAT 14-FEB-2003
DEFINITION	Sequence 143 from patent US 6127163.				
SEQUENCE	143				

Query Match	16.1%;	Score 15;	DB 6;	Length 41;
Best Local Similarity	67.7%;	Pred. No. 7.2e+05;		
Matches 21;	Conservative	0;	Mismatches 10;	Indels 0;
			Gaps	0;

```

QY      33 AATGCCTTGGTTTCACACTATCGGAATGTG 63
        ||| ||| ||| ||| ||| ||| ||| |||
Db      40 AATGCTTGAATTTAAGATGATGGGTATGAG 100

```

RESULT 49			
ARI47009/c			
LOCUS	ARI47009	41 bp	DNA
DEFINITION	Sequence 70 from patent US 6221561.		Linear
ACCESSION	ARI47009		

Query Match	16.1%;	Score 15;	DB 6;	Length 41;
Best Local Similarity	67.7%;	Pred. No. 7.2e+05;		
Matches 21; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0

```

Qy      33  AATGCCCTGGTTCAACACTATCGGAATGTG  63
          ||||| ||||| ||||| |||||
Db      40  AATGCTTGAATTTAAGATGATGGTATGAG  100

```

RESULT	50		
ARI58235/c			
LOCUS	ARI58235	41 bp	DNA
DEFINITION	Sequence 143 from patent US 6251403.		linear
ACCESSION	ARI58235		
			PMF 17-OCT-2001

FEATURES	location/Qualifier
source	1. .41
	/organism="unknown

BASE COUNT 13 a 12 c 3 g 13 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 41;
Best Local Similarity 67.7%; Pred. No. 7.2e+05;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 33 AATGCTTGGTTTCAACACTATCGCATG 63
||||| 11111 11111 11111 11111
Db 40 AATGCTTGAATTTAAGATGATGATGATG 10

RESULT 51

AR174250 41 bp DNA linear PAT 17-DEC-2001
LOCUS AR174250
DEFINITION Sequence 30 from patent US 6306649.
ACCESSION AR174250
VERSION AR174250.1 GI:17914570
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 41)
AUTHORS Gilman,M.Z. and Natesan,S.
TITLE Heterologous transcription factors
JOURNAL Patent: US 6306649-A 30 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..41

BASE COUNT 16 a 6 c 13 g 6 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 41;
Best Local Similarity 67.7%; Pred. No. 7.2e+05;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 45 TCACACTATGCGATCGACTGCGGCT 75
||||| 11111 11111 11111 11111
Db 5 TCACACTAGAGATGGCATGGAAGGCT 35

RESULT 52

AR033895 42 bp DNA linear PAT 29-SEP-1999
LOCUS AR033895
DEFINITION Sequence 38 from patent US 5869270.
ACCESSION AR033895
VERSION AR033895.1 GI:5949500
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
TITLE Single chain MHC complexes and uses thereof
JOURNAL Patent: US 5869270-A 38 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..42

BASE COUNT 6 a 20 c 11 g 5 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 42;
Best Local Similarity 67.7%; Pred. No. 7.3e+05;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCATTCCTGCGGTGACATGCTTG 41
||||| 11111 11111 11111 11111
Db 1 CCCCCAGGCTCCCGGCGCACCATGCCGTG 31

RESULT 53

AR175028 42 bp DNA linear PAT 17-DEC-2001
LOCUS AR175028

DEFINITION Sequence 38 from patent US 6309645.
ACCESSION AR175028
VERSION AR175028.1 GI:17916327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
TITLE MHC molecules and uses thereof
JOURNAL Patent: US 6309645-A 38 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..42

BASE COUNT 6 a 20 c 11 g 5 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 42;
Best Local Similarity 67.7%; Pred. No. 7.3e+05;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCATTCCTGCGGTGACATGCTTG 41
||||| 11111 11111 11111 11111
Db 1 CCCCCAGGCTCCCGGCGCACCATGCCGTG 31

RESULT 54

AX032460 42 bp DNA linear PAT 20-SEP-2000
LOCUS AX032460
DEFINITION Sequence 38 from Patent EP0997477.
ACCESSION AX032460
VERSION AX032460.1 GI:10279417
KEYWORDS
SOURCE unidentified.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Chavalliaz,P.A., Edwards,A.C., Grammer,S., Jiao,J.A., Rhode,P.R.,
Weidanz,J.A. and Wong,H.C.
TITLE Mhc complexes and uses thereof
JOURNAL Patent: EP 0997477-A 38 03-MAY-2000;
FEATURES Location/Qualifiers
source 1..42

BASE COUNT 6 a 20 c 11 g 5 t
ORIGIN

Query Match 16.1%; Score 15; DB 6; Length 42;
Best Local Similarity 67.7%; Pred. No. 7.3e+05;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCATTCCTGCGGTGACATGCTTG 41
||||| 11111 11111 11111 11111
Db 1 CCCCCAGGCTCCCGGCGCACCATGCCGTG 31

RESULT 55

AR161438 45 bp DNA linear PAT 17-OCT-2001
LOCUS AR161438
DEFINITION Sequence 13 from patent US 6255462.
ACCESSION AR161438
VERSION AR161438.1 GI:16227322
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Grose,C.F.
TITLE Peptide tag for immunodetection and immunopurification
JOURNAL Patent: US 6255462-A 13 03-JUL-2001;
FEATURES Location/Qualifiers

AR189580/c
 LOCUS AR189580 27 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 5068 from patent US 6346398.
 ACCESSION AR189580
 VERSION AR189580.1 GI:20235545
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Payco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 5068 12-FEB-2002;
 FEATURES
 source Location/Qualifiers
 BASE COUNT 9 a 5 c 4 g 8 t 1 others
 ORIGIN
 Query Match 15.9%; Score 14.8; DB 6; Length 27;
 Best Local Similarity 70.4%; Pred. No. 8.1e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 61 GTGACTGTCGGCCCTCCAGAAACATT 87
 ||||| ||| | ||||| |||||
 Db 27 GTGAGTGTTCNMCATCAGAAACATT 1

RESULT 61
 AX000160 27 bp DNA linear PAT 10-MAR-2000
 LOCUS AX000160
 DEFINITION Sequence 11 from Patent WO9906574.
 ACCESSION AX000160
 VERSION AX000160.1 GI:7240674
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Visser,J. and De,G.L.
 TITLE CELLULOSE DEGRADING ENZYMES OF ASPERGILLUS
 JOURNAL Patent: WO 9906574-A 11 11-FEB-1999;
 VISSEER JACOB (NL); GIELEKENS MARCUS MATHEUS CATHAR (NL)
 FEATURES
 source Location/Qualifiers
 BASE COUNT 8 a 10 c 2 g 7 t
 ORIGIN
 Query Match 15.9%; Score 14.8; DB 6; Length 27;
 Best Local Similarity 73.1%; Pred. No. 8.1e+05;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 31 ACAATGCCTTGTTTCAACACTATCG 56
 ||||| || | || || || || ||
 Db 2 ACAATGCATTCCTTCCAAATCTACG 27

RESULT 62
 AR086544 30 bp DNA linear PAT 07-SEP-2000
 LOCUS AR086544
 DEFINITION Sequence 33 from patent US 5985599.
 ACCESSION AR086544
 VERSION AR086544.1 GI:10013310
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS McKenzie,I.F.C., Hogarth,M.P., Hibbs,M.L., Scott,B.M., Bonadonna,L. and Hulett,M.D.

TITLE FC receptor for immunoglobulin
 JOURNAL Patent: US 5985599-A 33 16-NOV-1999;
 FEATURES
 source Location/Qualifiers
 BASE COUNT 8 a 6 c 7 g 9 t
 ORIGIN
 Query Match 15.9%; Score 14.8; DB 6; Length 30;
 Best Local Similarity 73.1%; Pred. No. 8.3e+05;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 44 TTCACACTATGCGAATGATGACATGTC 69
 ||||| ||||| ||| ||||| |||||
 Db 3 TTCTAGACTATGCGACAGTATGATGTC 28

RESULT 63
 AX034592/c 36 bp DNA linear PAT 22-SEP-2000
 LOCUS AX034592
 DEFINITION Sequence 5 from Patent EP0865495.
 ACCESSION AX034592
 VERSION AX034592.1 GI:10303185
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Wats,C.K. and Hamilton,J.A.
 TITLE Progestin-regulated gene
 JOURNAL Patent: EP 0865495-A 5 23-SEP-1998;
 GARVAN INSR MED RES (AU)
 FEATURES
 source Location/Qualifiers
 BASE COUNT 7 a 9 c 10 g 10 t
 ORIGIN
 Query Match 15.9%; Score 14.8; DB 6; Length 36;
 Best Local Similarity 88.9%; Pred. No. 8.5e+05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 73 CCTCCAGAAACATTGAG 90
 ||||| ||||| ||||| |||||
 Db 29 CCTCCAGGAACACTGAG 12

RESULT 64
 AX407350 36 bp DNA linear PAT 14-JUN-2002
 LOCUS AX407350
 DEFINITION Sequence 12 from Patent WO0224929.
 ACCESSION AX407350
 VERSION AX407350.1 GI:21440055
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Ehrlich,R., Rotem-Yehudai,R. and Laham,N.
 TITLE A soluble beta 2 microglobulin (betazm)/hfe monochain for biotechnological and therapeutic applications
 JOURNAL Patent: WO 0224929-A 12 28-MAR-2002;
 Ramot University Authority for Applied Research & Industrial Dev LTD. (IL)
 FEATURES
 source Location/Qualifiers
 BASE COUNT 9 a 11 c 12 g 4 t

Query Match 15.9%; Score 14.8; DB 6; Length 36;
Best Local Similarity 73.1%; Pred. No. 8.5e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 68 TCGGGCTCCAGAAACATTCGAGG 93
||| || ||||| ||| |||||
DB 11 TCGAGCTCCCGATCAGATGAGGGG 36

RESULT 65
AX219418
LOCUS AX219418 38 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 4860 from Patent WO0159103.
ACCESSION AX219418
VERSION AX219418.1 GI:15547442
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Blatt, L., McSwigen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 4860 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwigen, James (US); Chowrira, Bharat M. (US)
FEATURES
source 1.38
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleic Acid"
modified_base 31
BASE COUNT 12 a 9 c 10 g 6 t 1 others
ORIGIN

Query Match 15.9%; Score 14.8; DB 6; Length 38;
Best Local Similarity 62.9%; Pred. No. 8.6e+05;
Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 51 CTATCGAATGATGATGCGGCTCCGCAAAACA 85
||||| ||||| ||||| |||||
DB 4 CTATCTGATGAGCGCGTATGCGCAANCAACA 38

RESULT 66
AR200843
LOCUS AR200843 41 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 147 from patent US 6358686.
ACCESSION AR200843
VERSION AR200843.1 GI:20251731
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Lemieux, B., Landry, B.S. and Sapolsky, R.J.
TITLE Brassica polymorphisms
JOURNAL Patent: US 6358686-A 147 19-MAR-2002;
FEATURES
source 1.41
/organism="unknown"
BASE COUNT 10 a 11 c 8 g 11 t 1 others
ORIGIN

Query Match 15.9%; Score 14.8; DB 6; Length 41;
Best Local Similarity 61.1%; Pred. No. 8.7e+05;
Matches 22; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

OY 28 GTGACATGCTTGTTCACACTATCGGATG 63
||||| ||||| ||||| |||||
DB 6 GTGAAAGCATGTGCTCAAAATCTCGCTGCG 41

RESULT 67
AX199548/c
LOCUS AX199548 44 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 478 from Patent WO0151670.
ACCESSION AX199548
VERSION AX199548.1 GI:15389973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 44)
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 478 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1.44
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 19
/note="2 of 2 allelic variants (477 is other entry)"
Accession number c943321506"
BASE COUNT 6 a 13 c 17 g 8 t
ORIGIN

Query Match 15.9%; Score 14.8; DB 6; Length 44;
Best Local Similarity 64.7%; Pred. No. 8.8e+05;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 46 CACACTATGGAATGTGCTGCGCTCCAG 79
||| || ||||| ||| |||||
DB 44 CAGCTCTGCGGAGGCTTCGCGCAGCGCTCCAG 11

RESULT 68
E06872
LOCUS E06872 45 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA related to milk growth hormone.
ACCESSION E06872.1 GI:2175037
VERSION E06872.1 GI:2175037
KEYWORDS JP 1994070776-A/1.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 45)
AUTHORS Harada, Y., Nakano, E., Tatsumi, H. and Umetsu, M.
TITLE NEW RECOMBINANT DNA, PRODUCTION OF MILK GROWTH HORMONE AND DNA
FRAGMENT FOR GENE SECRETION MANIFESTATION
JOURNAL Patent: JP 1994070776-A 1 15-MAR-1994;
KIRKOMAN CORP
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1994070776-A/1
PD 15-MAR-1994
PF 26-AUG-1992 JP 1992227507
PI HARADA YASUHIRO, NAKANO EIICHI, TATSUMI HIROKI, UMETSU MOTOAKI
PC C12N15/18, C12P21/02, (C12P21/02, C12R1:865);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.

FEATURES
source 1.45
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 4 a 18 c 10 g 13 t
ORIGIN

Query Match 15.9%; Score 14.8; DB 6; Length 45;

Best Local Similarity 88.9%; Pred. No. 9e+05; Mismatches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 56 GGATGTGACTGTGGGC 73
IIIIIIIIIIIIIIIIII
DB 4 GGATGTGACTGTGGGC 21

RESULT 76

AX003680/c

LOCUS AX003680 21 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 6 from Patent WO927091.
ACCESSION AX003680
VERSION AX003680.1 GI:9927467

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

LUNA SUSANA DE (ES); THANGUE NICHOLAS BARRIE (GB)

Location/Qualifiers

1..21

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Primer"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 81.0%; Pred. No. 9.4e+05;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 67 GTGGGCTCCAGAAACATT 87

IIIIIIIIIIIIIIIIII

DB 21 GTGGGCTCCAGAAACATT 1

RESULT 77

AX118607/c

LOCUS AX118607 21 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3730 from Patent WO0129262.
ACCESSION AX118607
VERSION AX118607.1 GI:14035558

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Orchid Biosciences, Inc. (US)

Location/Qualifiers

1..21

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Primer"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 81.0%; Pred. No. 9.4e+05;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 71 GGCTCCAGAAACATTGAGC 91

IIIIIIIIIIIIIIIIII

DB 21 GGCTCCAGAAACATTGAGC 1

RESULT 78

LOCUS A11495 30 bp DNA linear PAT 01-DEC-1993
DEFINITION Nucleotide sequence 35 from patent number EP0170204.
ACCESSION A11495
VERSION A11495.1 GI:492479

QY 8 GAGACTCCATTCGCTGGG 28
IIIIIIIIIIIIIIIIII

RESULT 79

A11499

LOCUS A11499 30 bp DNA linear PAT 01-DEC-1993
DEFINITION Nucleotide sequence 39 from patent number EP0170204.
ACCESSION A11499
VERSION A11499.1 GI:492483

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BOEHRINGER INGELHEIM INTERNATIONAL GmbH

Location/Qualifiers

1..30

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 81.0%; Pred. No. 9.9e+05;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GAGACTCCATTCGCTGGG 28

IIIIIIIIIIIIIIIIII

DB 10 GAGACTCCATTCGCTGGG 30

RESULT 80

A11501

LOCUS A11501 30 bp DNA linear PAT 01-DEC-1993
DEFINITION Nucleotide sequence 41 from patent number EP0170204.
ACCESSION A11501
VERSION A11501.1 GI:492485

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BOEHRINGER INGELHEIM INTERNATIONAL GmbH

Location/Qualifiers

1..30

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 81.0%; Pred. No. 9.9e+05;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GAGACTCCATTCGCTGGG 28

IIIIIIIIIIIIIIIIII

DB 10 GAGACTCCATTCGCTGGG 30

RESULT 81

A11501

unidentified.

ACCESSION AR209865
VERSION AR209865.1 GI:21511947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Gottschling, D.E. and Singer, M.S.
TITLE Telomerase compositions and methods
JOURNAL Patent: US 6387619-A 9 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..40
BASE COUNT 14 a 10 c 9 g 7 t
ORIGIN
Query Match 15.7%; Score 14.6; DB 6; Length 40;
Best Local Similarity 69.0%; Pred. No. 1e+06;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
CY 63 GACTGTGGGCTCCAGAAACATTGAG 91
Db 6 GACTGTGGGCTCCAGAAACATTGAG 34
RESULT 90
AX201867 40 bp DNA PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 13 from Patent W00153346.
ACCESSION AX201867
VERSION AX201867.1 GI:15391708
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mosseman, S. and Spek van Der, P.J.
TITLE Human cysteine knot polypeptide
JOURNAL Patent: WO 0153346-A 13 26-JUL-2001;
FEATURES Location/Qualifiers
source 1..40
BASE COUNT 10 a 9 c 10 g 11 t
ORIGIN
Query Match 15.7%; Score 14.6; DB 6; Length 40;
Best Local Similarity 69.0%; Pred. No. 1e+06;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
CY 48 ACATATCGAATGACTGCGGCCCTC 76
Db 12 ACATATGCGCATGAAGCTGCATCTC 40
RESULT 91
I85801 40 bp DNA linear PAT 10-JUN-1998
LOCUS
DEFINITION Sequence 9 from patent US 5698686.
ACCESSION I85801
VERSION I85801.1 GI:3205519
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Gottschling, D.E. and Singer, M.S.
TITLE Yeast telomerase compositions
JOURNAL Patent: US 5698686-A 9 16-DEC-1997;
FEATURES Location/Qualifiers
source 1..40

BASE COUNT 14 a 10 c 9 g 7 t
ORIGIN
Query Match 15.7%; Score 14.6; DB 6; Length 40;
Best Local Similarity 69.0%; Pred. No. 1e+06;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
CY 63 GACTGTGGGCTCCAGAAACATTGAG 91
Db 6 GACTGTGGGCTCCAGAAACATTGAG 34
RESULT 92
AR003527 45 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 4 from patent US 5744311.
ACCESSION AR003527
VERSION AR003527.1 GI:3964786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Fraiser, M.S., Spargo, C.A., Walker, G., Terrance, Van Cleave, M.,
Wright, D., James, and Little, M.C.
TITLE Strand displacement amplification using thermophilic enzymes
JOURNAL Patent: US 5744311-A 4 28-APR-1998;
FEATURES Location/Qualifiers
source 1..45
BASE COUNT 13 a 12 c 10 g 10 t
ORIGIN
Query Match 15.7%; Score 14.6; DB 6; Length 45;
Best Local Similarity 62.2%; Pred. No. 1e+06;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
CY 34 ATGCGTTGGTTTCACACTATCGAATGCTGCTG 70
Db 39 ATGCGTTGGTTTCACACTATCGAATGCTGCTG 3
RESULT 93
AX201009 45 bp DNA linear PAT 29-AUG-2001
LOCUS
DEFINITION Sequence 639 from Patent W00151633.
ACCESSION AX201009
VERSION AX201009.1 GI:15390830
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 45)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
JOURNAL Patent: WO 0151633-A 639 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..45
BASE COUNT 7 a 10 c 16 g 12 t
ORIGIN
Query Match 15.7%; Score 14.6; DB 6; Length 45;
Best Local Similarity 57.8%; Pred. No. 1e+06;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 31 ACAATGCTTGGTTCAACACTATCGAATGTGACTGCGGCGCT 75
 DB 1 AGAATGCTACCGTCTGCACTGCGTGAACGTCGTGCT 45

RESULT 94
 AX267808 45 bp DNA linear PAT 26-OCT-2001
 LOCUS Sequence 782 from Patent WO0173032.
 DEFINITION AX267808
 ACCESSION AX267808
 VERSION AX267808.1 GI:16516472
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Katos, M.D., Fanger, G.R., Retter, M.W., Stolk, D.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T. and Henderson, R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: WO 0173032-A 782 04-OCT-2001.
 CORIAX CORPORATION (US)

FEATURES
 source 1..45
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 7 a 10 c 16 g 12 t
 ORIGIN

Query Match 15.7%; Score 14.6; DB 6; Length 45;
 Best Local Similarity 57.8%; Pred. No. 1.1e+06;
 Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 31 ACAATGCTTGGTTCAACACTATCGAATGTGACTGCGGCGCT 75
 DB 1 AGAATGCTACCGTCTGCACTGCGTGAACGTCGTGCT 45

RESULT 95
 I55640 45 bp DNA linear PAT 07-OCT-1997
 LOCUS Sequence 4 from patent US 5648211.
 DEFINITION I55640
 ACCESSION I55640
 VERSION I55640.1 GI:2476434
 KEYWORDS unknown.
 SOURCE unknown.
 ORGANISM unknown.
 REFERENCE 1 (bases 1 to 45)
 Fraiser, M.S., Spargo, C.A., Walker, G., Terrance, Van Cleve, M., Wright, D., James, and Little, M.C.
 TITLE Strand displacement amplification using thermophilic enzymes
 JOURNAL Patent: US 5648211-A 4 15-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..45
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BASE COUNT 13 a 12 c 10 g 10 t
 ORIGIN

Query Match 15.7%; Score 14.6; DB 6; Length 45;
 Best Local Similarity 62.2%; Pred. No. 1.1e+06;
 Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 34 ATGCGTTGGTTCAACACTATCGAATGTGACTGCG 70
 DB 39 ATGCTTCCTGTAACCGAGTAGATTGGGACTATTG 3

RESULT 96
 HSTCELL13/c

LOCUS HSTCELL13 45 bp DNA linear PRI 11-MAY-1995
 DEFINITION H.sapiens rearranged TCR alpha chain variable region (Val3.1Ja42).
 ACCESSION X81548
 VERSION X81548.1 GI:550351
 KEYWORDS joining region; T cell receptor; Tcell alpha chain; variable region.

SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 45)
 Davodeau, F.
 TITLE Direct Submission
 JOURNAL Submitted (19-SEP-1994) F. Davodeau, INSERM U 211, INSERM U 211, Inst. de Biologie, 9, Quai Moncousu, 44035 Nantes Cedex, FRANCE
 REFERENCE 2 (bases 1 to 45)
 Davodeau, F., Peyrat, M.A., Gaschet, J., Hallet, M.M., Triebe, F., Vie, H., Kabeitz, D. and Bonneville, M.
 TITLE Surface expression of functional T cell receptor chains formed by interlocus recombination on human T lymphocytes
 JOURNAL J. Exp. Med. 180 (5), 1685-1691 (1994)
 MEDLINE 95053700
 PUBMED 7964454

FEATURES
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 /organism="Homo sapiens"
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 /note="contains part of the V, and J region"

V_region
 BASE COUNT 12 a 6 c 15 g 12 t
 ORIGIN

Query Match 15.7%; Score 14.6; DB 9; Length 45;
 Best Local Similarity 69.0%; Pred. No. 1.1e+06;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

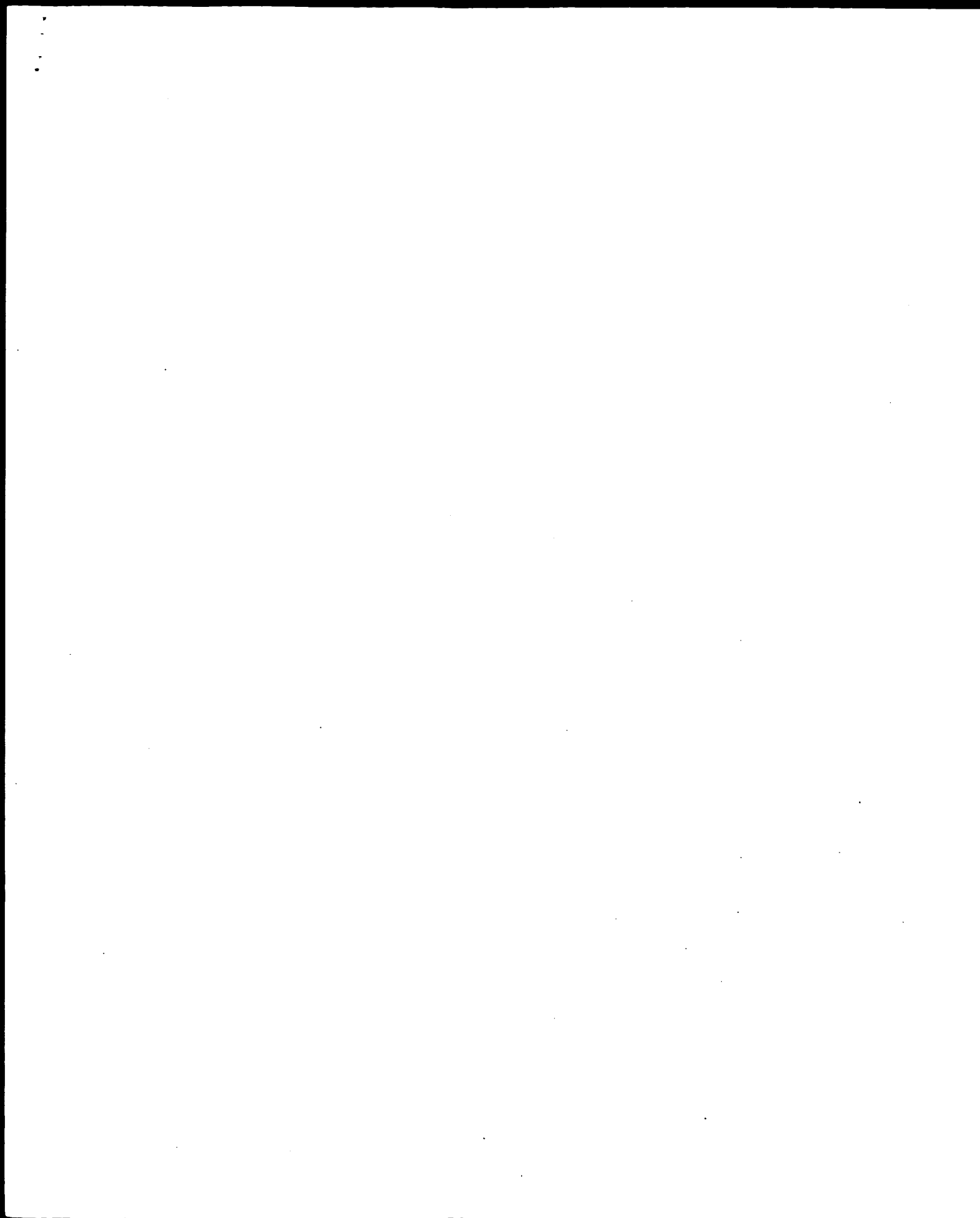
QY 27 GGTGACATGCTTGGTTCAACACTATC 55
 DB 42 GATGATTTCTCTCTCAATATGCTCTCATATC 14

RESULT 97
 AR052850 47 bp DNA linear PAT 29-SEP-1999
 LOCUS Sequence 187 from patent US 5833975.
 DEFINITION AR052850
 ACCESSION AR052850
 VERSION AR052850.1 GI:5977712
 KEYWORDS unknown.
 SOURCE unknown.
 ORGANISM unknown.
 REFERENCE 1 (bases 1 to 47)
 Paoletti, E., Tartaglia, J. and Cox, W.I.
 TITLE Canaripox virus expressing cytokine and/or tumor-associated antigen
 JOURNAL Patent: US 5833975-A 187 10-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..47
 /organism="unknown"

BASE COUNT 8 a 9 c 14 g 16 t
 ORIGIN

Query Match 15.7%; Score 14.6; DB 6; Length 47;
 Best Local Similarity 57.8%; Pred. No. 1.1e+06;
 Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 35 TGCCTTGGTTCAACACTATCGAATGTGACTGCGGCGCTCAG 79
 DB 3 TGGTGTGTAGTCTCTCAAAATGTGCTCGAGAGCTGCTG 47



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OM nucleic - nucleic search, using sw model

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Title: US-09-843-377-3_COPY_1000_1092

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Searched: 1085931 seqs, 780495707 residues

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Listing first 1000 summaries

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.						
1	16.2	17.4	31	10	US-09-993-110-22	Sequence 22, Appl
2	16.2	17.4	50	7	US-08-781-986A-2630	Sequence 2630, Ap
3	16	17.2	43	9	US-09-801-371A-2	Sequence 2, Appl1
4	16	17.2	43	9	US-09-801-371A-6	Sequence 6, Appl1
5	16	17.2	43	9	US-09-801-371A-8	Sequence 8, Appl1
6	15.8	17.0	25	9	US-10-098-263B-78554	Sequence 78554, A
7	15.8	17.0	35	9	US-10-158-735-10	Sequence 10, Appl
8	15.8	17.0	42	9	US-10-043-573-45	Sequence 45, Appl
9	15.6	16.8	25	9	US-10-215-112-1028	Sequence 1028, Ap
10	15.6	16.8	25	9	US-10-215-112-3613	Sequence 1513, Ap
11	15.2	16.3	31	10	US-09-801-371A-694	Sequence 694, Appl
12	15.2	16.3	46	10	US-09-872-696A-40	Sequence 40, Appl
13	15.2	16.3	46	10	US-09-231-235-40	Sequence 40, Appl
14	15.2	16.3	46	10	US-09-797-518A-40	Sequence 15, Appl
15	15	16.1	15	9	US-09-935-280-15	Sequence 5, Appl1
16	15	16.1	16	9	US-10-003-021-5	Sequence 1, Appl1
17	15	16.1	16	10	US-09-792-875-1	Sequence 7295, Ap
18	15	16.1	25	9	US-10-098-263B-7295	Sequence 35881, A
19	15	16.1	25	9	US-10-098-263B-35881	Sequence 506, App

c 93	14	15.1	32	9	US-10-029-314-20	Sequence 20, Appl	c 166	13.8	14.8	25	9	US-10-098-263B-126512	Sequence 126512,
94	14	15.1	32	9	US-10-029-314-21	Sequence 21, Appl	c 167	13.8	14.8	26	9	US-09-919-501-9	Sequence 9, Appl1
c 95	14	15.1	32	9	US-09-899-732-20	Sequence 20, Appl	c 168	13.8	14.8	27	9	US-10-174-513-3	Sequence 3, Appl1
c 96	14	15.1	32	9	US-09-899-732-21	Sequence 21, Appl	c 169	13.8	14.8	27	10	US-09-897-798-3	Sequence 12, Appl1
c 97	14	15.1	32	10	US-09-885-478-20	Sequence 20, Appl	c 170	13.8	14.8	35	9	US-10-032-241A-12	Sequence 12, Appl
c 98	14	15.1	32	10	US-09-885-478-21	Sequence 21, Appl	c 171	13.8	14.8	36	10	US-09-731-393-13	Sequence 97, Appl
c 99	14	15.1	34	9	US-10-102-949-2	Sequence 2, Appl1	c 172	13.8	14.8	44	9	US-09-840-277-97	Sequence 6, Appl1
c 100	14	15.1	39	9	US-10-005-956-1436	Sequence 1436, Ap	c 173	13.8	14.8	47	9	US-09-989-975-6	Sequence 73, Appl1
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102	14	15.1	43	10	US-09-733-246-81	Sequence 81, Appl	c 175	13.6	14.6	20	9	US-09-824-322B-468	Sequence 21932, A
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104	14	15.1	45	9	US-09-902-853-234	Sequence 234, App	c 177	13.6	14.6	25	9	US-10-098-263B-21992	Sequence 22805, A
105	14	15.1	45	9	US-09-907-824-234	Sequence 234, App	c 178	13.6	14.6	25	9	US-10-098-263B-22825	Sequence 31000, A
106	14	15.1	45	9	US-09-907-841-234	Sequence 234, App	c 179	13.6	14.6	25	9	US-10-098-263B-31000	Sequence 35039, A
107	14	15.1	45	9	US-09-904-011-234	Sequence 234, App	c 180	13.6	14.6	25	9	US-10-098-263B-35039	Sequence 50087, A
108	14	15.1	45	9	US-09-906-742-234	Sequence 234, App	c 181	13.6	14.6	25	9	US-10-098-263B-5107	Sequence 51707, A
109	14	15.1	45	9	US-09-906-888-234	Sequence 234, App	c 182	13.6	14.6	25	9	US-10-098-263B-5107	Sequence 51707, A
110	14	15.1	45	9	US-09-907-613-234	Sequence 234, App	c 183	13.6	14.6	25	9	US-10-098-263B-5698	Sequence 79644, A
111	14	15.1	45	9	US-09-907-942-234	Sequence 234, App	c 184	13.6	14.6	25	9	US-10-098-263B-79964	Sequence 103751, A
112	14	15.1	45	9	US-09-904-820-234	Sequence 234, App	c 185	13.6	14.6	25	9	US-10-098-263B-103751	Sequence 110980, A
113	14	15.1	45	9	US-09-904-859-234	Sequence 234, App	c 186	13.6	14.6	25	9	US-10-098-263B-110980	Sequence 1379, Ap
114	14	15.1	45	9	US-09-909-204-234	Sequence 234, App	c 187	13.6	14.6	29	9	US-09-864-636A-1379	Sequence 1379, Ap
115	14	15.1	45	9	US-09-904-786-234	Sequence 234, App	c 188	13.6	14.6	29	10	US-09-745-763-154	Sequence 154, Ap
116	14	15.1	45	9	US-09-906-646-234	Sequence 234, App	c 189	13.6	14.6	30	9	US-09-953-052-60	Sequence 60, Appl
117	14	15.1	45	9	US-09-906-700-234	Sequence 234, App	c 190	13.6	14.6	30	9	US-10-085-906-133	Sequence 133, Appl
118	14	15.1	45	9	US-09-902-903-234	Sequence 234, App	c 191	13.6	14.6	33	9	US-10-096-125-23	Sequence 6250, Ap
119	14	15.1	45	9	US-09-903-749A-234	Sequence 234, App	c 192	13.6	14.6	37	9	US-09-848-754A-6250	Sequence 6250, Ap
120	14	15.1	45	9	US-09-903-786-234	Sequence 234, App	c 193	13.6	14.6	37	9	US-10-156-306-6252	Sequence 6283, Ap
121	14	15.1	45	9	US-09-902-736-234	Sequence 234, App	c 194	13.6	14.6	37	9	US-10-156-306-6283	Sequence 2036, Ap
122	14	15.1	45	9	US-09-904-119-234	Sequence 234, App	c 195	13.6	14.6	38	9	US-09-776-474-0036	Sequence 3, Appl1
123	14	15.1	45	9	US-09-904-956-234	Sequence 234, App	c 196	13.6	14.6	39	9	US-10-023-711-3	Sequence 4, Appl1
124	14	15.1	45	9	US-09-907-794-234	Sequence 234, App	c 197	13.6	14.6	42	10	US-09-969-139-4	Sequence 5, Appl1
125	14	15.1	45	9	US-09-908-741-42	Sequence 42, Appl	c 198	13.6	14.6	42	10	US-09-969-139-5	Sequence 356, Appl
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157	13.8	14.8	25	9	US-10-098-263B-21010	Sequence 21010, A	c 230	13.6	14.6	46	9	US-09-907-575-356	Sequence 356, App
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c 162	13.8	14.8	25	9	US-10-098-263B-116213	Sequence 116213, A	c 235	13.6	14.6	46	9	US-09-907-919-356	Sequence 356, App
c 163	13.8	14.8	25	9	US-10-098-263B-117240	Sequence 117240, A	c 236	13.6	14.6	46	9	US-09-902-615-356	Sequence 356, App
c 164	13.8	14.8	25	9	US-10-098-263B-120825	Sequence 120825, A	c 237	13.6	14.6	46	9	US-09-903-925-356	Sequence 356, App
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241	13.6	14.6	46	9	US-09-907-652-356	Sequence 356, App	C 314	13.2	14.2	25	9	US-10-098-263B-24130	Sequence 24130, A
242	13.6	14.6	46	9	US-09-902-572A-356	Sequence 356, App	C 315	13.2	14.2	25	9	US-10-098-263B-38821	Sequence 38821, A
243	13.6	14.6	46	9	US-09-902-979-356	Sequence 356, App	C 316	13.2	14.2	25	9	US-10-098-263B-45825	Sequence 45825, A
244	13.6	14.6	46	9	US-09-905-125-356	Sequence 356, App	C 317	13.2	14.2	25	9	US-10-098-263B-46453	Sequence 46453, A
245	13.6	14.6	46	9	US-09-906-815A-356	Sequence 356, App	C 318	13.2	14.2	25	9	US-10-098-263B-55207	Sequence 55207, A
246	13.6	14.6	46	10	US-09-284-663A-19	Sequence 19, App	C 319	13.2	14.2	25	9	US-10-098-263B-64803	Sequence 64803, A
247	13.6	14.6	46	10	US-09-909-320-356	Sequence 356, App	C 320	13.2	14.2	25	9	US-10-098-263B-72681	Sequence 72681, A
248	13.6	14.6	46	10	US-09-909-088B-356	Sequence 288, App	C 321	13.2	14.2	25	9	US-10-098-263B-99221	Sequence 99221, A
249	13.6	14.6	48	10	US-09-922-261-288	Sequence 1804, App	C 322	13.2	14.2	25	9	US-10-098-263B-99729	Sequence 99729, A
250	13.6	14.6	50	7	US-08-781-986A-1804	Sequence 307, App	C 323	13.2	14.2	25	9	US-10-098-263B-104169	Sequence 104169, A
251	13.4	14.4	20	8	US-08-983-603-307	Sequence 1804, App	C 324	13.2	14.2	25	9	US-10-098-263B-107964	Sequence 107964, A
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253	13.4	14.4	25	9	US-10-215-112-5166	Sequence 5166, App	C 326	13.2	14.2	25	9	US-10-098-263B-124849	Sequence 124849, A
254	13.4	14.4	25	9	US-10-098-263B-7296	Sequence 7296, App	C 327	13.2	14.2	25	9	US-10-098-263B-124850	Sequence 124850, A
255	13.4	14.4	25	9	US-10-098-263B-17967	Sequence 17967, A	C 328	13.2	14.2	28	10	US-09-452-999-99	Sequence 99, App
256	13.4	14.4	25	9	US-10-098-263B-17968	Sequence 17968, A	C 329	13.2	14.2	28	10	US-09-949-145-59	Sequence 59, App
257	13.4	14.4	25	9	US-10-098-263B-35631	Sequence 18694, A	C 330	13.2	14.2	29	9	US-09-864-656A-173	Sequence 5, App
258	13.4	14.4	25	9	US-10-098-263B-35631	Sequence 35631, A	C 331	13.2	14.2	29	9	US-09-864-656A-173	Sequence 173, App
259	13.4	14.4	25	9	US-10-098-263B-35631	Sequence 35631, A	C 332	13.2	14.2	29	9	US-09-864-656A-909	Sequence 909, App
260	13.4	14.4	25	9	US-10-098-263B-35631	Sequence 35631, A	C 333	13.2	14.2	29	9	US-10-087-775-8	Sequence 8, App
261	13.4	14.4	25	9	US-10-098-263B-43970	Sequence 43970, A	C 334	13.2	14.2	30	9	US-09-764-868B-1246	Sequence 1246, App
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264	13.4	14.4	25	9	US-10-098-263B-66159	Sequence 66159, A	C 337	13.2	14.2	31	9	US-09-848-754A-5948	Sequence 486, App
265	13.4	14.4	25	9	US-10-098-263B-66159	Sequence 66159, A	C 338	13.2	14.2	31	9	US-10-084-814-19	Sequence 19, App
266	13.4	14.4	25	9	US-10-098-263B-66159	Sequence 66159, A	C 339	13.2	14.2	31	10	US-09-801-874-1048	Sequence 1048, App
267	13.4	14.4	25	9	US-10-098-263B-89909	Sequence 89909, A	C 340	13.2	14.2	32	9	US-10-035-098-6	Sequence 6, App
268	13.4	14.4	25	9	US-10-098-263B-98692	Sequence 98692, A	C 341	13.2	14.2	32	9	US-10-083-168-102	Sequence 102, App
269	13.4	14.4	25	9	US-10-098-263B-98692	Sequence 98692, A	C 342	13.2	14.2	35	9	US-09-987-755-4	Sequence 4, App
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272	13.4	14.4	25	10	US-09-768-436-39	Sequence 121461, A	C 345	13.2	14.2	37	9	US-09-848-754A-9454	Sequence 9454, App
273	13.4	14.4	25	10	US-09-866-108-5064	Sequence 5064, App	C 346	13.2	14.2	37	9	US-10-224-836-200	Sequence 200, App
274	13.4	14.4	25	10	US-09-866-108-5067	Sequence 5067, App	C 347	13.2	14.2	38	9	US-09-780-533A-4559	Sequence 4559, App
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276	13.4	14.4	31	9	US-09-771-382-41	Sequence 41, App	C 349	13.2	14.2	38	9	US-09-848-754A-4441	Sequence 4441, App
277	13.4	14.4	31	9	US-10-024-659-3	Sequence 3, App	C 350	13.2	14.2	38	10	US-10-156-306-1119	Sequence 1119, App
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280	13.4	14.4	37	9	US-09-770-158-14	Sequence 14, App	C 353	13.2	14.2	39	10	US-09-966-217-23	Sequence 23, App
281	13.4	14.4	38	9	US-09-770-158-13	Sequence 13, App	C 354	13.2	14.2	43	9	US-09-966-217-24	Sequence 24, App
282	13.4	14.4	38	10	US-09-884-877-4	Sequence 4, App	C 355	13.2	14.2	43	9	US-09-966-930-24	Sequence 24, App
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288	13.4	14.4	42	9	US-09-940-244-19	Sequence 19, App	C 361	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
289	13.4	14.4	42	9	US-09-940-925A-19	Sequence 19, App	C 362	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
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298	13.4	14.4	48	9	US-09-864-785-3513	Sequence 3513, App	C 371	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
299	13.4	14.4	48	9	US-09-780-533A-6318	Sequence 6318, App	C 372	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
300	13.4	14.4	48	9	US-09-780-533A-6504	Sequence 6504, App	C 373	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
301	13.4	14.4	48	9	US-09-780-533A-6504	Sequence 6504, App	C 374	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
302	13.4	14.4	48	9	US-09-780-533A-6504	Sequence 6504, App	C 375	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
303	13.4	14.4	48	9	US-09-780-533A-6504	Sequence 6504, App	C 376	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
304	13.4	14.4	48	10	US-09-910-120-73	Sequence 73, App	C 377	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
305	13.4	14.4	50	9	US-10-211-239-4	Sequence 4, App	C 378	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
306	13.2	14.2	20	9	US-09-824-322B-354	Sequence 354, App	C 379	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
307	13.2	14.2	21	9	US-09-998-425-61	Sequence 61, App	C 380	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
308	13.2	14.2	21	9	US-09-997-977-61	Sequence 61, App	C 381	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
309	13.2	14.2	21	10	US-09-961-848-19	Sequence 19, App	C 382	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
310	13.2	14.2	22	10	US-10-216-993-221	Sequence 221, App	C 383	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App
311	13.2	14.2	25	9	US-10-215-112-11647	Sequence 11647, A	C 384	13.2	14.2	45	9	US-09-905-291A-219	Sequence 219, App

385	13.2	14.2	45	9	US-09-903-943-219	Sequence 219, App	C 458	13.2	14.2	50	9	US-09-903-786-302	Sequence 302, App
386	13.2	14.2	45	9	US-09-904-462-219	Sequence 219, App	C 459	13.2	14.2	50	9	US-09-903-786-302	Sequence 302, App
387	13.2	14.2	45	9	US-09-905-056-219	Sequence 219, App	C 460	13.2	14.2	50	9	US-09-902-736-302	Sequence 302, App
388	13.2	14.2	45	9	US-09-907-925-219	Sequence 219, App	C 461	13.2	14.2	50	9	US-09-902-736-302	Sequence 302, App
389	13.2	14.2	45	9	US-09-904-553-219	Sequence 219, App	C 462	13.2	14.2	50	9	US-09-904-119-345	Sequence 345, App
390	13.2	14.2	45	9	US-09-905-381-219	Sequence 219, App	C 463	13.2	14.2	50	9	US-09-904-119-345	Sequence 345, App
391	13.2	14.2	45	9	US-09-909-064-219	Sequence 219, App	C 464	13.2	14.2	50	9	US-09-904-956-302	Sequence 302, App
392	13.2	14.2	45	9	US-09-905-088-219	Sequence 219, App	C 465	13.2	14.2	50	9	US-09-904-956-302	Sequence 302, App
393	13.2	14.2	45	9	US-09-907-575-219	Sequence 219, App	C 466	13.2	14.2	50	9	US-09-907-794-345	Sequence 345, App
394	13.2	14.2	45	9	US-09-907-759-219	Sequence 219, App	C 467	13.2	14.2	50	9	US-09-907-794-345	Sequence 345, App
395	13.2	14.2	45	9	US-09-905-075-219	Sequence 219, App	C 468	13.2	14.2	50	9	US-09-902-692-345	Sequence 345, App
396	13.2	14.2	45	9	US-09-902-634-219	Sequence 219, App	C 469	13.2	14.2	50	9	US-09-902-692-345	Sequence 345, App
397	13.2	14.2	45	9	US-09-902-713-219	Sequence 219, App	C 470	13.2	14.2	50	9	US-09-903-520-345	Sequence 345, App
398	13.2	14.2	45	9	US-09-907-979-219	Sequence 219, App	C 471	13.2	14.2	50	9	US-09-903-520-345	Sequence 345, App
399	13.2	14.2	45	9	US-09-902-615-219	Sequence 219, App	C 472	13.2	14.2	50	9	US-09-903-943-302	Sequence 302, App
400	13.2	14.2	45	9	US-09-903-925-219	Sequence 219, App	C 473	13.2	14.2	50	9	US-09-903-943-302	Sequence 302, App
401	13.2	14.2	45	9	US-09-906-760A-219	Sequence 219, App	C 474	13.2	14.2	50	9	US-09-904-462-345	Sequence 345, App
402	13.2	14.2	45	9	US-09-903-823-219	Sequence 219, App	C 475	13.2	14.2	50	9	US-09-904-462-345	Sequence 345, App
403	13.2	14.2	45	9	US-09-907-652-219	Sequence 219, App	C 476	13.2	14.2	50	9	US-09-905-056-302	Sequence 302, App
404	13.2	14.2	45	9	US-09-902-572A-219	Sequence 219, App	C 477	13.2	14.2	50	9	US-09-905-056-345	Sequence 345, App
405	13.2	14.2	45	9	US-09-902-979-219	Sequence 219, App	C 478	13.2	14.2	50	9	US-09-907-925-302	Sequence 302, App
406	13.2	14.2	45	9	US-09-905-125-219	Sequence 219, App	C 479	13.2	14.2	50	9	US-09-907-925-345	Sequence 345, App
407	13.2	14.2	45	9	US-09-906-815A-219	Sequence 219, App	C 480	13.2	14.2	50	9	US-09-904-553-302	Sequence 302, App
408	13.2	14.2	45	10	US-09-909-320-219	Sequence 219, App	C 481	13.2	14.2	50	9	US-09-904-553-345	Sequence 345, App
409	13.2	14.2	45	10	US-09-909-088B-219	Sequence 219, App	C 482	13.2	14.2	50	9	US-09-905-381-302	Sequence 302, App
410	13.2	14.2	47	9	US-09-853-526-332	Sequence 232, App	C 483	13.2	14.2	50	9	US-09-905-381-345	Sequence 345, App
411	13.2	14.2	47	9	US-09-853-526-309	Sequence 309, App	C 484	13.2	14.2	50	9	US-09-909-064-302	Sequence 302, App
412	13.2	14.2	47	9	US-09-966-277-45	Sequence 45, App	C 485	13.2	14.2	50	9	US-09-909-064-345	Sequence 345, App
413	13.2	14.2	47	9	US-09-966-277-46	Sequence 46, App	C 486	13.2	14.2	50	9	US-09-905-088-345	Sequence 345, App
414	13.2	14.2	47	9	US-09-966-930-45	Sequence 45, App	C 487	13.2	14.2	50	9	US-09-905-088-345	Sequence 345, App
415	13.2	14.2	47	9	US-09-966-930-46	Sequence 46, App	C 488	13.2	14.2	50	9	US-09-907-575-302	Sequence 302, App
416	13.2	14.2	47	9	US-09-918-156-63	Sequence 63, App	C 489	13.2	14.2	50	9	US-09-907-575-345	Sequence 345, App
417	13.2	14.2	47	10	US-09-901-484A-232	Sequence 309, App	C 490	13.2	14.2	50	9	US-09-902-759-302	Sequence 302, App
418	13.2	14.2	47	10	US-09-901-484A-309	Sequence 309, App	C 491	13.2	14.2	50	9	US-09-902-759-345	Sequence 345, App
419	13.2	14.2	47	12	US-09-994-420-1	Sequence 1, App	C 492	13.2	14.2	50	9	US-09-905-075-302	Sequence 302, App
420	13.2	14.2	47	12	US-09-082-032-1	Sequence 1, App	C 493	13.2	14.2	50	9	US-09-905-075-345	Sequence 345, App
421	13.2	14.2	48	9	US-09-918-156-1	Sequence 1, App	C 494	13.2	14.2	50	9	US-09-902-634-302	Sequence 302, App
422	13.2	14.2	48	10	US-09-910-120-70	Sequence 70, App	C 495	13.2	14.2	50	9	US-09-902-634-345	Sequence 345, App
423	13.2	14.2	49	9	US-10-122-706-14	Sequence 14, App	C 496	13.2	14.2	50	9	US-09-902-713-302	Sequence 302, App
424	13.2	14.2	50	9	US-09-905-291A-302	Sequence 302, App	C 497	13.2	14.2	50	9	US-09-902-713-345	Sequence 345, App
425	13.2	14.2	50	9	US-09-905-291A-345	Sequence 345, App	C 498	13.2	14.2	50	9	US-09-907-979-302	Sequence 302, App
426	13.2	14.2	50	9	US-09-902-853-302	Sequence 302, App	C 499	13.2	14.2	50	9	US-09-907-979-345	Sequence 345, App
427	13.2	14.2	50	9	US-09-902-853-345	Sequence 345, App	C 500	13.2	14.2	50	9	US-09-902-615-302	Sequence 302, App
428	13.2	14.2	50	9	US-09-907-824-302	Sequence 302, App	C 501	13.2	14.2	50	9	US-09-902-615-345	Sequence 345, App
429	13.2	14.2	50	9	US-09-907-824-345	Sequence 345, App	C 502	13.2	14.2	50	9	US-09-903-925-302	Sequence 302, App
430	13.2	14.2	50	9	US-09-907-841-302	Sequence 302, App	C 503	13.2	14.2	50	9	US-09-903-925-345	Sequence 345, App
431	13.2	14.2	50	9	US-09-907-841-345	Sequence 345, App	C 504	13.2	14.2	50	9	US-09-906-760A-302	Sequence 302, App
432	13.2	14.2	50	9	US-09-904-011-302	Sequence 302, App	C 505	13.2	14.2	50	9	US-09-906-760A-345	Sequence 345, App
433	13.2	14.2	50	9	US-09-904-011-345	Sequence 345, App	C 506	13.2	14.2	50	9	US-09-903-823-302	Sequence 302, App
434	13.2	14.2	50	9	US-09-906-742-302	Sequence 302, App	C 507	13.2	14.2	50	9	US-09-903-823-345	Sequence 345, App
435	13.2	14.2	50	9	US-09-906-742-345	Sequence 345, App	C 508	13.2	14.2	50	9	US-09-907-652-302	Sequence 302, App
436	13.2	14.2	50	9	US-09-906-838-302	Sequence 302, App	C 509	13.2	14.2	50	9	US-09-907-652-345	Sequence 345, App
437	13.2	14.2	50	9	US-09-906-838-345	Sequence 345, App	C 510	13.2	14.2	50	9	US-09-902-572A-302	Sequence 302, App
438	13.2	14.2	50	9	US-09-907-613-302	Sequence 302, App	C 511	13.2	14.2	50	9	US-09-902-572A-345	Sequence 345, App
439	13.2	14.2	50	9	US-09-907-613-345	Sequence 345, App	C 512	13.2	14.2	50	9	US-09-902-979-302	Sequence 302, App
440	13.2	14.2	50	9	US-09-907-942-302	Sequence 302, App	C 513	13.2	14.2	50	9	US-09-902-979-345	Sequence 345, App
441	13.2	14.2	50	9	US-09-907-942-345	Sequence 345, App	C 514	13.2	14.2	50	9	US-09-905-125-302	Sequence 302, App
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443	13.2	14.2	50	9	US-09-904-820-345	Sequence 345, App	C 516	13.2	14.2	50	9	US-09-906-815A-302	Sequence 302, App
444	13.2	14.2	50	9	US-09-904-859-302	Sequence 302, App	C 517	13.2	14.2	50	9	US-09-906-815A-345	Sequence 345, App
445	13.2	14.2	50	9	US-09-904-859-345	Sequence 345, App	C 518	13.2	14.2	50	10	US-09-909-320-302	Sequence 302, App
446	13.2	14.2	50	9	US-09-909-204-302	Sequence 302, App	C 519	13.2	14.2	50	10	US-09-909-320-345	Sequence 345, App
447	13.2	14.2	50	9	US-09-909-204-345	Sequence 345, App	C 520	13.2	14.2	50	10	US-09-909-088B-302	Sequence 302, App
448	13.2	14.2	50	9	US-09-904-786-302	Sequence 302, App	C 521	13.2	14.2	50	10	US-09-909-088B-345	Sequence 345, App
449	13.2	14.2	50	9	US-09-904-786-345	Sequence 345, App	C 522	13	14.0	21	10	US-09-777-789-80	Sequence 80, App
450	13.2	14.2	50	9	US-09-906-646-302	Sequence 302, App	C 523	13	14.0	21	10	US-09-752-154-2	Sequence 2, App
451	13.2	14.2	50	9	US-09-906-646-345	Sequence 345, App	C 524	13	14.0	23	10	US-09-745-317-11	Sequence 11, App
452	13.2	14.2	50	9	US-09-906-700-302	Sequence 302, App	C 525	13	14.0	23	10	US-09-923-246-103	Sequence 103, App
453	13.2	14.2	50	9	US-09-906-700-345	Sequence 345, App	C 526	13	14.0	24	10	US-09-940-185-792	Sequence 279, App
454	13.2	14.2	50	9	US-09-902-903-302	Sequence 302, App	C 527	13	14.0	24	10	US-09-992-860-4	Sequence 4, App
455	13.2	14.2	50	9	US-09-902-903-345	Sequence 345, App	C 528	13	14.0	25	9	US-09-734-853A-753	Sequence 753, App
456	13.2	14.2	50	9	US-09-903-749A-302	Sequence 302, App	C 529	13	14.0	25	9	US-10-215-112-716	Sequence 716, App
457	13.2	14.2	50	9	US-09-903-749A-345	Sequence 345, App	C 530	13	14.0	25	9	US-10-215-112-546	Sequence 2546, App

531	13	14.0	25	9	US-10-215-112-8532	Sequence 8532, Ap	604	13	14.0	50	9	US-09-905-291A-135	Sequence 135, App
532	13	14.0	25	9	US-10-098-263B-3368	Sequence 3368, Ap	605	13	14.0	50	9	US-09-902-883-135	Sequence 135, App
533	13	14.0	25	9	US-10-098-263B-13243	Sequence 13243, A	606	13	14.0	50	9	US-09-907-824-135	Sequence 135, App
534	13	14.0	25	9	US-10-098-263B-17513	Sequence 17513, A	607	13	14.0	50	9	US-09-907-841-135	Sequence 135, App
535	13	14.0	25	9	US-10-098-263B-21090	Sequence 21090, A	608	13	14.0	50	9	US-09-904-011-135	Sequence 135, App
536	13	14.0	25	9	US-10-098-263B-40832	Sequence 40832, A	609	13	14.0	50	9	US-09-906-742-135	Sequence 135, App
537	13	14.0	25	9	US-10-098-263B-49283	Sequence 49283, A	610	13	14.0	50	9	US-09-906-888-135	Sequence 135, App
538	13	14.0	25	9	US-10-098-263B-53034	Sequence 53034, A	611	13	14.0	50	9	US-09-907-613-135	Sequence 135, App
539	13	14.0	25	9	US-10-098-263B-55400	Sequence 55400, A	612	13	14.0	50	9	US-09-907-942-135	Sequence 135, App
540	13	14.0	25	9	US-10-098-263B-58486	Sequence 58486, A	613	13	14.0	50	9	US-09-904-820-135	Sequence 135, App
541	13	14.0	25	9	US-10-098-263B-62198	Sequence 62198, A	614	13	14.0	50	9	US-09-904-859-135	Sequence 135, App
542	13	14.0	25	9	US-10-098-263B-71165	Sequence 71165, A	615	13	14.0	50	9	US-09-904-204-135	Sequence 135, App
543	13	14.0	25	9	US-10-098-263B-79242	Sequence 79242, A	616	13	14.0	50	9	US-09-904-786-135	Sequence 135, App
544	13	14.0	25	9	US-10-098-263B-98315	Sequence 98315, A	617	13	14.0	50	9	US-09-906-646-135	Sequence 135, App
545	13	14.0	25	9	US-10-098-263B-99101	Sequence 99101, A	618	13	14.0	50	9	US-09-906-700-135	Sequence 135, App
546	13	14.0	25	9	US-10-098-263B-99728	Sequence 99728, A	619	13	14.0	50	9	US-09-902-903-135	Sequence 135, App
547	13	14.0	25	9	US-10-098-263B-127266	Sequence 127266, A	620	13	14.0	50	9	US-09-903-786-135	Sequence 135, App
548	13	14.0	25	9	US-09-866-108-5062	Sequence 5062, Ap	622	13	14.0	50	9	US-09-902-716-135	Sequence 135, App
549	13	14.0	25	10	US-09-866-108-5063	Sequence 5063, Ap	623	13	14.0	50	9	US-09-904-119-135	Sequence 135, App
550	13	14.0	25	10	US-09-866-108-5068	Sequence 5068, Ap	624	13	14.0	50	9	US-09-904-956-135	Sequence 135, App
551	13	14.0	25	10	US-09-866-108-5069	Sequence 5069, Ap	625	13	14.0	50	9	US-09-907-794-135	Sequence 135, App
552	13	14.0	25	10	US-09-866-108-5069	Sequence 5069, Ap	626	13	14.0	50	9	US-09-902-692-135	Sequence 135, App
553	13	14.0	26	9	US-09-281-495-41	Sequence 41, Appl	627	13	14.0	50	9	US-09-903-520-135	Sequence 135, App
554	13	14.0	26	10	US-09-755-665-75	Sequence 75, Appl	628	13	14.0	50	9	US-09-903-943-135	Sequence 135, App
555	13	14.0	29	9	US-10-172-867-5	Sequence 5, Appl	629	13	14.0	50	9	US-09-904-462-135	Sequence 135, App
556	13	14.0	30	10	US-09-878-756-8	Sequence 8, Appl	630	13	14.0	50	9	US-09-905-056-135	Sequence 135, App
557	13	14.0	31	9	US-09-971-631-18	Sequence 18, Appl	631	13	14.0	50	9	US-09-907-925-135	Sequence 135, App
558	13	14.0	31	10	US-09-801-274-1247	Sequence 1247, Ap	632	13	14.0	50	9	US-09-904-553-135	Sequence 135, App
559	13	14.0	31	10	US-09-801-274-1327	Sequence 1327, Ap	633	13	14.0	50	9	US-09-905-381-135	Sequence 135, App
560	13	14.0	33	9	US-10-219-246-32	Sequence 32, Appl	634	13	14.0	50	9	US-09-909-064-135	Sequence 135, App
561	13	14.0	33	9	US-10-219-247-32	Sequence 24, Appl	635	13	14.0	50	9	US-09-905-068-135	Sequence 135, App
562	13	14.0	33	9	US-10-241-476-24	Sequence 24, Appl	636	13	14.0	50	9	US-09-902-575-135	Sequence 135, App
563	13	14.0	33	9	US-10-105-200A-52	Sequence 52, Appl	637	13	14.0	50	9	US-09-902-759-135	Sequence 135, App
564	13	14.0	33	9	US-10-105-504A-52	Sequence 52, Appl	638	13	14.0	50	9	US-09-905-075-135	Sequence 135, App
565	13	14.0	33	9	US-10-105-678A-52	Sequence 52, Appl	639	13	14.0	50	9	US-09-902-634-135	Sequence 135, App
566	13	14.0	33	9	US-09-990-586-70	Sequence 70, Appl	640	13	14.0	50	9	US-09-902-713-135	Sequence 135, App
567	13	14.0	33	9	US-09-990-586-71	Sequence 71, Appl	641	13	14.0	50	9	US-09-907-979-135	Sequence 135, App
568	13	14.0	33	10	US-09-835-722-32	Sequence 32, Appl	642	13	14.0	50	9	US-10-282-121-8	Sequence 135, App
569	13	14.0	33	10	US-09-817-774-10	Sequence 10, Appl	643	13	14.0	50	9	US-09-903-925-135	Sequence 135, App
570	13	14.0	34	9	US-09-995-593A-24	Sequence 24, Appl	644	13	14.0	50	9	US-09-902-615-135	Sequence 135, App
571	13	14.0	34	9	US-09-965-131-4	Sequence 4, Appl	645	13	14.0	50	9	US-09-906-760A-135	Sequence 135, App
572	13	14.0	35	9	US-09-993-164-19	Sequence 19, Appl	646	13	14.0	50	9	US-09-903-823-135	Sequence 135, App
573	13	14.0	35	9	US-10-216-981A-10	Sequence 10, Appl	647	13	14.0	50	9	US-09-907-652-135	Sequence 135, App
574	13	14.0	35	10	US-09-803-165-1	Sequence 1, Appl	648	13	14.0	50	9	US-09-902-512A-135	Sequence 135, App
575	13	14.0	37	9	US-10-004-633-25	Sequence 25, Appl	649	13	14.0	50	9	US-09-902-979-135	Sequence 135, App
576	13	14.0	37	9	US-09-848-753A-6274	Sequence 6274, Ap	650	13	14.0	50	9	US-09-905-125-135	Sequence 135, App
577	13	14.0	38	9	US-09-825-805-1220	Sequence 1220, Ap	651	13	14.0	50	9	US-09-906-815A-135	Sequence 135, App
578	13	14.0	38	9	US-09-780-533A-3610	Sequence 3610, Ap	652	13	14.0	50	10	US-09-954-166-6	Sequence 135, App
579	13	14.0	38	9	US-09-780-533A-4239	Sequence 4239, Ap	653	13	14.0	50	10	US-09-909-120-135	Sequence 135, App
580	13	14.0	38	9	US-09-780-533A-4800	Sequence 4800, Ap	654	13	14.0	50	10	US-09-909-188B-135	Sequence 135, App
581	13	14.0	40	9	US-09-466-035-80	Sequence 80, Appl	655	13	14.0	50	10	US-09-864-785-184	Sequence 184, App
582	13	14.0	40	9	US-09-466-035-81	Sequence 81, Appl	656	13	14.0	50	9	US-09-739-909-2	Sequence 2, Appl
583	13	14.0	40	9	US-09-997-931-104	Sequence 104, App	657	13	14.0	50	9	US-09-776-474-900	Sequence 900, App
584	13	14.0	40	10	US-09-238-351-23	Sequence 23, Appl	658	13	14.0	17	9	US-09-776-474-900	Sequence 900, App
585	13	14.0	40	10	US-09-919-855-6	Sequence 6, Appl	659	13	14.0	17	10	US-09-790-017-17	Sequence 17, App
586	13	14.0	40	10	US-09-912-679-81	Sequence 81, Appl	660	13	14.0	20	9	US-10-007-078-135	Sequence 70, Appl
587	13	14.0	42	9	US-10-121-256-66	Sequence 66, Appl	661	13	14.0	21	9	US-09-232-785-10	Sequence 13, Appl
588	13	14.0	44	9	US-10-193-960-61	Sequence 61, Appl	662	13	14.0	22	9	US-09-970-820-13	Sequence 13, Appl
589	13	14.0	44	9	US-09-900-379-40	Sequence 40, Appl	663	13	14.0	22	9	US-09-986-718-13	Sequence 13, Appl
590	13	14.0	44	10	US-09-848-164-40	Sequence 40, Appl	664	13	14.0	22	9	US-10-004-633-130	Sequence 20, Appl
591	13	14.0	46	10	US-09-834-109-13	Sequence 13, Appl	665	13	14.0	22	9	US-09-899-980A-16	Sequence 16, Appl
592	13	14.0	46	10	US-09-943-722-39	Sequence 39, Appl	666	13	14.0	22	10	US-09-371-900-13	Sequence 4, Appl
593	13	14.0	48	9	US-09-991-209-8	Sequence 8, Appl	667	13	14.0	22	10	US-09-940-155-1959	Sequence 1959, Ap
594	13	14.0	48	9	US-09-877-478-5831	Sequence 5831, Ap	668	13	14.0	24	9	US-10-060-756A-3211	Sequence 3211, Ap
595	13	14.0	48	9	US-09-848-753A-8244	Sequence 8244, Ap	669	13	14.0	25	9	US-10-215-112-142	Sequence 142, App
596	13	14.0	48	9	US-09-848-753A-8310	Sequence 8310, Ap	670	13	14.0	25	9	US-10-215-112-1717	Sequence 1717, Ap
597	13	14.0	48	9	US-09-930-423-4335	Sequence 4335, Ap	671	13	14.0	25	9	US-10-215-112-327	Sequence 2327, Ap
598	13	14.0	48	9	US-10-156-306-7518	Sequence 7518, Ap	672	13	14.0	25	9	US-10-215-112-6727	Sequence 6727, Ap
599	13	14.0	48	12	US-09-975-408-70	Sequence 70, Appl	673	13	14.0	25	9	US-10-215-112-10731	Sequence 10731, A
600	13	14.0	49	9	US-10-075-559-70	Sequence 70, Appl	674	13	14.0	25	9		
601	13	14.0	49	9	US-10-087-523-42	Sequence 42, Appl	675	13	14.0	25	9		
602	13	14.0	49	9	US-09-912-077-14	Sequence 14, Appl	676	13	14.0	25	9		
603	13	14.0	49	9	US-10-101-030B-50	Sequence 50, Appl	677	13	14.0	25	9		

c 677	12.8	13.8	25	9	US-10-215-112-13396	Sequence 13396, A	750	12.8	13.8	42	9	US-09-895-793-787	Sequence 787, App
c 678	12.8	13.8	25	9	US-10-215-112-13760	Sequence 13760, A	751	12.8	13.8	42	9	US-09-895-814-787	Sequence 787, App
c 679	12.8	13.8	25	9	US-10-098-263B-4407	Sequence 4407, Ap	752	12.8	13.8	42	9	US-09-954-594A-26	Sequence 26, Appl
c 680	12.8	13.8	25	9	US-10-098-263B-4663	Sequence 4663, Ap	753	12.8	13.8	42	9	US-09-974-685-26	Sequence 26, Appl
c 681	12.8	13.8	25	9	US-10-098-263B-4949	Sequence 4949, Ap	754	12.8	13.8	42	9	US-10-197-185-26	Sequence 26, Appl
c 682	12.8	13.8	25	9	US-10-098-263B-5661	Sequence 5661, Ap	755	12.8	13.8	42	10	US-09-759-143-787	Sequence 787, App
c 683	12.8	13.8	25	9	US-10-098-263B-16248	Sequence 16248, A	756	12.8	13.8	42	10	US-09-780-669-787	Sequence 787, App
c 684	12.8	13.8	25	9	US-10-098-263B-16266	Sequence 16266, A	757	12.8	13.8	42	10	US-09-865-807-26	Sequence 26, Appl
c 685	12.8	13.8	25	9	US-10-098-263B-20025	Sequence 20025, A	758	12.8	13.8	42	10	US-09-822-827-787	Sequence 787, App
c 686	12.8	13.8	25	9	US-10-098-263B-21425	Sequence 21425, A	759	12.8	13.8	43	9	US-09-943-722-107	Sequence 107, Appl
c 687	12.8	13.8	25	9	US-10-098-263B-24479	Sequence 24479, A	760	12.8	13.8	44	10	US-09-775-925-19	Sequence 19, Appl
c 688	12.8	13.8	25	9	US-10-098-263B-27334	Sequence 27334, A	761	12.8	13.8	45	9	US-10-012-986-786	Sequence 786, App
c 689	12.8	13.8	25	9	US-10-098-263B-30716	Sequence 30716, A	762	12.8	13.8	45	9	US-09-895-793-786	Sequence 786, App
c 690	12.8	13.8	25	9	US-10-098-263B-41156	Sequence 41156, A	763	12.8	13.8	45	9	US-09-895-814-786	Sequence 786, App
c 691	12.8	13.8	25	9	US-10-098-263B-44370	Sequence 44370, A	764	12.8	13.8	45	9	US-09-954-987B-141	Sequence 141, App
c 692	12.8	13.8	25	9	US-10-098-263B-50770	Sequence 50770, A	765	12.8	13.8	45	9	US-09-954-987B-142	Sequence 142, App
c 693	12.8	13.8	25	9	US-10-098-263B-57828	Sequence 57828, A	766	12.8	13.8	45	10	US-09-759-143-786	Sequence 786, App
c 694	12.8	13.8	25	9	US-10-098-263B-60110	Sequence 60110, A	767	12.8	13.8	45	10	US-09-780-669-786	Sequence 786, App
c 695	12.8	13.8	25	9	US-10-098-263B-62714	Sequence 62714, A	768	12.8	13.8	45	9	US-09-822-827-786	Sequence 786, App
c 696	12.8	13.8	25	9	US-10-098-263B-62742	Sequence 62742, A	769	12.8	13.8	46	9	US-09-922-588-239	Sequence 239, App
c 697	12.8	13.8	25	9	US-10-098-263B-68461	Sequence 68461, A	770	12.8	13.8	46	9	US-09-988-293A-239	Sequence 239, App
c 698	12.8	13.8	25	9	US-10-098-263B-84309	Sequence 84309, A	771	12.8	13.8	46	9	US-09-988-735-239	Sequence 239, App
c 699	12.8	13.8	25	9	US-10-098-263B-84311	Sequence 84311, A	772	12.8	13.8	46	9	US-09-990-444-239	Sequence 239, App
c 700	12.8	13.8	25	9	US-10-098-263B-86277	Sequence 86277, A	773	12.8	13.8	46	9	US-09-989-730-239	Sequence 239, App
c 701	12.8	13.8	25	9	US-10-098-263B-86625	Sequence 86625, A	774	12.8	13.8	46	9	US-09-990-436-239	Sequence 239, App
c 702	12.8	13.8	25	9	US-10-098-263B-88035	Sequence 88035, A	775	12.8	13.8	46	9	US-09-991-181-239	Sequence 239, App
c 703	12.8	13.8	25	9	US-10-098-263B-88718	Sequence 88718, A	776	12.8	13.8	46	9	US-09-993-687-239	Sequence 239, App
c 704	12.8	13.8	25	9	US-10-098-263B-89792	Sequence 89792, A	777	12.8	13.8	46	9	US-09-989-724-239	Sequence 239, App
c 705	12.8	13.8	25	9	US-10-098-263B-90682	Sequence 90682, A	778	12.8	13.8	46	9	US-09-997-653-239	Sequence 239, App
c 706	12.8	13.8	25	9	US-10-098-263B-97584	Sequence 97584, A	779	12.8	13.8	46	9	US-09-993-667-239	Sequence 239, App
c 707	12.8	13.8	25	9	US-10-098-263B-99886	Sequence 99886, A	780	12.8	13.8	46	9	US-09-990-438-239	Sequence 239, App
c 708	12.8	13.8	25	9	US-10-098-263B-111530	Sequence 111530, A	781	12.8	13.8	46	9	US-09-990-562-239	Sequence 239, App
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c 710	12.8	13.8	25	9	US-10-098-263B-117174	Sequence 117174, A	783	12.8	13.8	46	9	US-09-997-666-239	Sequence 239, App
c 711	12.8	13.8	25	9	US-10-098-263B-119306	Sequence 119306, A	784	12.8	13.8	46	9	US-09-990-711-239	Sequence 239, App
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c 713	12.8	13.8	25	9	US-10-098-263B-123356	Sequence 123356, A	786	12.8	13.8	46	9	US-09-990-427-239	Sequence 239, App
c 714	12.8	13.8	25	9	US-10-098-263B-124576	Sequence 124576, A	787	12.8	13.8	46	9	US-09-998-156-239	Sequence 239, App
c 715	12.8	13.8	25	9	US-10-098-263B-127436	Sequence 127436, A	788	12.8	13.8	46	9	US-09-991-157-239	Sequence 239, App
c 716	12.8	13.8	25	10	US-09-866-108-4050	Sequence 4051, Ap	789	12.8	13.8	46	9	US-09-991-172-239	Sequence 239, App
c 717	12.8	13.8	25	10	US-09-885-441-31	Sequence 4051, Ap	790	12.8	13.8	46	9	US-09-997-514-239	Sequence 239, App
c 718	12.8	13.8	27	9	US-10-243-035-4	Sequence 41, Appl	791	12.8	13.8	46	9	US-09-990-443-239	Sequence 239, App
c 719	12.8	13.8	29	9	US-09-746-783-60	Sequence 60, Appl	792	12.8	13.8	46	9	US-09-990-726-239	Sequence 239, App
c 720	12.8	13.8	29	9	US-10-313-852-20	Sequence 20, Appl	793	12.8	13.8	46	9	US-09-997-559-239	Sequence 239, App
c 721	12.8	13.8	29	9	US-10-314-033-20	Sequence 20, Appl	794	12.8	13.8	46	9	US-09-997-601-239	Sequence 239, App
c 722	12.8	13.8	29	10	US-09-795-232-3	Sequence 3, Appl	795	12.8	13.8	46	9	US-09-989-729A-239	Sequence 239, App
c 723	12.8	13.8	31	9	US-09-858-560-11	Sequence 11, Appl	796	12.8	13.8	46	9	US-09-993-469-239	Sequence 239, App
c 724	12.8	13.8	31	9	US-09-847-172-11	Sequence 176, App	797	12.8	13.8	46	9	US-09-993-748-239	Sequence 239, App
c 725	12.8	13.8	31	10	US-09-801-274-176	Sequence 491, App	798	12.8	13.8	46	9	US-09-991-854-239	Sequence 239, App
c 726	12.8	13.8	31	10	US-09-801-274-491	Sequence 869, App	799	12.8	13.8	46	9	US-09-997-349-239	Sequence 239, App
c 727	12.8	13.8	31	10	US-09-801-274-869	Sequence 1374, Ap	800	12.8	13.8	46	9	US-09-997-628-239	Sequence 239, App
c 728	12.8	13.8	31	10	US-09-801-274-1374	Sequence 1784, Ap	801	12.8	13.8	46	9	US-09-997-683-239	Sequence 239, App
c 729	12.8	13.8	31	10	US-09-801-274-1784	Sequence 323, App	802	12.8	13.8	46	9	US-09-993-469-239	Sequence 239, App
c 730	12.8	13.8	31	10	US-09-765-272-323	Sequence 4, Appl	803	12.8	13.8	46	9	US-09-993-748-239	Sequence 239, App
c 731	12.8	13.8	33	9	US-09-880-729-4	Sequence 87, Appl	804	12.8	13.8	46	9	US-09-997-542-239	Sequence 239, App
c 732	12.8	13.8	33	9	US-09-891-943-87	Sequence 87, Appl	805	12.8	13.8	46	9	US-09-990-427-239	Sequence 239, App
c 733	12.8	13.8	33	9	US-10-236-629-1	Sequence 8, Appl	806	12.8	13.8	46	9	US-09-990-439-239	Sequence 239, App
c 734	12.8	13.8	33	9	US-10-236-629-8	Sequence 14, Appl	807	12.8	13.8	46	9	US-09-989-338-239	Sequence 239, App
c 735	12.8	13.8	33	9	US-10-236-629-14	Sequence 87, Appl	808	12.8	13.8	46	9	US-09-993-563-239	Sequence 239, App
c 736	12.8	13.8	33	10	US-09-350-629-87	Sequence 10, Appl	809	12.8	13.8	46	9	US-09-941-992-239	Sequence 239, App
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c 739	12.8	13.8	36	10	US-09-504-231A-2221	Sequence 47, Appl	812	12.8	13.8	46	9	US-09-997-585-239	Sequence 239, App
c 740	12.8	13.8	36	10	US-09-484-704-47	Sequence 2221, Ap	813	12.8	13.8	46	9	US-09-998-041-239	Sequence 239, App
c 741	12.8	13.8	36	10	US-09-274-553D-2221	Sequence 3025, Ap	814	12.8	13.8	46	10	US-09-989-722-239	Sequence 239, App
c 742	12.8	13.8	36	10	US-09-854-799-12	Sequence 12, Appl	815	12.8	13.8	46	10	US-09-989-727-239	Sequence 239, App
c 743	12.8	13.8	36	10	US-09-877-478-1025	Sequence 38, Appl	816	12.8	13.8	46	10	US-09-989-731-239	Sequence 239, App
c 744	12.8	13.8	38	9	US-09-981-803-38	Sequence 163, App	817	12.8	13.8	46	10	US-09-989-733-239	Sequence 239, App
c 745	12.8	13.8	40	9	US-10-123-071-13	Sequence 787, App	818	12.8	13.8	46	10	US-09-991-073-239	Sequence 239, App
c 746	12.8	13.8	40	9	US-09-848-616-163		819	12.8	13.8	46	10		
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c 749	12.8	13.8	42	9			822	12.8	13.8	46	10		

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C 824	12.8	13.8	46	10	US-09-991-163-239	Sequence 239, App	897	12.6	13.5	31	9	US-10-007-452-27	Sequence 27, Appl
C 825	12.8	13.8	46	10	US-09-993-604-239	Sequence 239, App	898	12.6	13.5	32	10	US-09-875-519A-4	Sequence 4, Appl
C 826	12.8	13.8	46	10	US-09-990-456-239	Sequence 239, App	C 899	12.6	13.5	32	10	US-09-875-519A-7	Sequence 7, Appl
C 827	12.8	13.8	46	10	US-09-989-721-239	Sequence 239, App	C 900	12.6	13.5	32	10	US-09-875-519A-10	Sequence 10, Appl
C 828	12.8	13.8	47	9	US-09-853-526-212	Sequence 212, App	C 901	12.6	13.5	32	10	US-09-982-610A-54	Sequence 54, Appl
C 829	12.8	13.8	47	9	US-10-001-054-90	Sequence 90, Appl	C 902	12.6	13.5	33	9	US-09-978-240A-54	Sequence 44, Appl
C 830	12.8	13.8	47	9	US-09-782-974C-177	Sequence 177, App	C 903	12.6	13.5	34	10	US-09-761-116-27	Sequence 27, Appl
C 831	12.8	13.8	47	10	US-09-901-484A-212	Sequence 212, App	C 904	12.6	13.5	35	10	US-09-765-272-278	Sequence 278, App
C 832	12.8	13.8	47	10	US-09-916-940-55	Sequence 55, Appl	C 905	12.6	13.5	35	10	US-09-844-268-9	Sequence 9, Appl
C 833	12.8	13.8	47	10	US-09-916-940-55	Sequence 55, Appl	C 906	12.6	13.5	35	10	US-09-844-268-9	Sequence 9, Appl
C 834	12.8	13.8	47	10	US-09-918-601-53	Sequence 13, Appl	C 907	12.6	13.5	36	9	US-10-164-163-7	Sequence 7, Appl
C 835	12.8	13.8	48	9	US-09-848-754A-8260	Sequence 8260, App	C 908	12.6	13.5	36	10	US-09-950-255-3	Sequence 3, Appl
C 836	12.8	13.8	48	9	US-09-782-974C-148	Sequence 148, App	C 909	12.6	13.5	36	10	US-09-904-599A-13	Sequence 13, Appl
C 837	12.8	13.8	49	9	US-10-138-838-59	Sequence 59, Appl	C 910	12.6	13.5	37	10	US-09-878-454A-13	Sequence 13, Appl
C 838	12.8	13.8	49	9	US-10-139-031-59	Sequence 59, Appl	C 911	12.6	13.5	38	9	US-10-036-041-70	Sequence 70, Appl
C 839	12.8	13.8	49	9	US-10-138-905-59	Sequence 59, Appl	C 912	12.6	13.5	38	9	US-10-035-855-70	Sequence 70, Appl
C 840	12.8	13.8	49	9	US-10-138-916-59	Sequence 59, Appl	C 913	12.6	13.5	38	9	US-09-931-834-70	Sequence 70, Appl
C 841	12.8	13.8	49	9	US-09-976-800-59	Sequence 59, Appl	C 914	12.6	13.5	38	9	US-10-036-214-70	Sequence 70, Appl
C 842	12.8	13.8	50	9	US-10-192-085-12	Sequence 12, Appl	C 915	12.6	13.5	38	9	US-10-035-719-70	Sequence 70, Appl
C 843	12.6	13.5	19	9	US-10-041-856-83	Sequence 83, Appl	C 916	12.6	13.5	38	9	US-10-036-160-70	Sequence 70, Appl
C 844	12.6	13.5	20	10	US-09-735-995-44	Sequence 44, Appl	C 917	12.6	13.5	38	9	US-09-730-289B-2187	Sequence 2187, App
C 845	12.6	13.5	25	9	US-10-215-112-1281	Sequence 1281, App	C 918	12.6	13.5	38	9	US-10-035-958-70	Sequence 70, Appl
C 846	12.6	13.5	25	9	US-10-215-112-6033	Sequence 6033, App	C 919	12.6	13.5	38	9	US-10-036-150-70	Sequence 70, Appl
C 847	12.6	13.5	25	9	US-10-215-112-6884	Sequence 6884, App	C 920	12.6	13.5	38	9	US-09-780-533A-3114	Sequence 3114, App
C 848	12.6	13.5	25	9	US-10-215-112-6950	Sequence 6950, App	C 921	12.6	13.5	38	9	US-09-877-478-3794	Sequence 3873, App
C 849	12.6	13.5	25	9	US-10-215-112-6950	Sequence 6950, App	C 922	12.6	13.5	38	9	US-09-848-754A-4286	Sequence 4286, App
C 850	12.6	13.5	25	9	US-10-215-112-10475	Sequence 10475, App	C 923	12.6	13.5	38	9	US-09-848-754A-4538	Sequence 4538, App
C 851	12.6	13.5	25	9	US-10-215-112-1109	Sequence 1109, App	C 924	12.6	13.5	38	9	US-09-776-474-1465	Sequence 1465, App
C 852	12.6	13.5	25	9	US-10-215-112-11872	Sequence 12872, App	C 925	12.6	13.5	38	9	US-09-776-474-1465	Sequence 1465, App
C 853	12.6	13.5	25	9	US-10-098-263B-682	Sequence 682, App	C 926	12.6	13.5	38	9	US-09-780-164-1275	Sequence 1275, App
C 854	12.6	13.5	25	9	US-10-098-263B-682	Sequence 682, App	C 927	12.6	13.5	38	9	US-09-780-164-1275	Sequence 1275, App
C 855	12.6	13.5	25	9	US-10-098-263B-9345	Sequence 9345, App	C 928	12.6	13.5	38	9	US-09-780-164-1284	Sequence 1284, App
C 856	12.6	13.5	25	9	US-10-098-263B-11727	Sequence 11727, App	C 929	12.6	13.5	38	9	US-09-930-423-2024	Sequence 2024, App
C 857	12.6	13.5	25	9	US-10-098-263B-12611	Sequence 12611, App	C 930	12.6	13.5	38	9	US-10-036-063-70	Sequence 70, Appl
C 858	12.6	13.5	25	9	US-10-098-263B-17788	Sequence 17788, App	C 931	12.6	13.5	38	9	US-10-156-306-686	Sequence 686, App
C 859	12.6	13.5	25	9	US-10-098-263B-20063	Sequence 20063, App	C 932	12.6	13.5	38	9	US-10-156-306-1095	Sequence 1095, App
C 860	12.6	13.5	25	9	US-10-098-263B-20222	Sequence 20222, App	C 933	12.6	13.5	38	10	US-10-036-342-70	Sequence 70, Appl
C 861	12.6	13.5	25	9	US-10-098-263B-29667	Sequence 29667, App	C 934	12.6	13.5	38	12	US-10-036-342-70	Sequence 70, Appl
C 862	12.6	13.5	25	9	US-10-098-263B-30414	Sequence 30414, App	C 935	12.6	13.5	39	9	US-09-309-136-99	Sequence 99, Appl
C 863	12.6	13.5	25	9	US-10-098-263B-44033	Sequence 44033, App	C 936	12.6	13.5	39	9	US-09-953-354-29	Sequence 29, Appl
C 864	12.6	13.5	25	9	US-10-098-263B-44034	Sequence 44034, App	C 937	12.6	13.5	39	10	US-09-263-959-187	Sequence 187, App
C 865	12.6	13.5	25	9	US-10-098-263B-50783	Sequence 50783, App	C 938	12.6	13.5	40	10	US-09-861-368-9	Sequence 9, Appl
C 866	12.6	13.5	25	9	US-10-098-263B-67786	Sequence 67786, App	C 939	12.6	13.5	41	9	US-10-043-573-111	Sequence 111, App
C 867	12.6	13.5	25	9	US-10-098-263B-78123	Sequence 78123, App	C 940	12.6	13.5	41	9	US-10-043-573-122	Sequence 122, App
C 868	12.6	13.5	25	9	US-10-098-263B-79511	Sequence 79511, App	C 941	12.6	13.5	42	9	US-09-954-594A-21	Sequence 21, Appl
C 869	12.6	13.5	25	9	US-10-098-263B-79511	Sequence 79511, App	C 942	12.6	13.5	42	9	US-09-974-685-21	Sequence 21, Appl
C 870	12.6	13.5	25	9	US-10-098-263B-89765	Sequence 89765, App	C 943	12.6	13.5	42	9	US-10-139-480-9	Sequence 9, Appl
C 871	12.6	13.5	25	9	US-10-098-263B-10162	Sequence 10162, App	C 944	12.6	13.5	42	9	US-10-116-298A-27	Sequence 27, Appl
C 872	12.6	13.5	25	9	US-10-098-263B-101780	Sequence 101780, App	C 945	12.6	13.5	42	9	US-10-197-185-21	Sequence 21, Appl
C 873	12.6	13.5	25	9	US-10-098-263B-110307	Sequence 110307, App	C 946	12.6	13.5	43	10	US-09-865-807-21	Sequence 21, Appl
C 874	12.6	13.5	25	9	US-10-098-263B-111551	Sequence 111551, App	C 947	12.6	13.5	43	9	US-10-023-066A-94	Sequence 94, Appl
C 875	12.6	13.5	25	9	US-10-098-263B-118013	Sequence 118013, App	C 948	12.6	13.5	43	9	US-09-869-339-40	Sequence 40, Appl
C 876	12.6	13.5	25	10	US-09-827-998-1696	Sequence 1696, App	C 949	12.6	13.5	43	9	US-09-890-586-32	Sequence 32, Appl
C 877	12.6	13.5	25	10	US-09-827-998-1697	Sequence 1697, App	C 950	12.6	13.5	46	9	US-09-978-295A-440	Sequence 440, App
C 878	12.6	13.5	25	10	US-09-827-998-1698	Sequence 1698, App	C 951	12.6	13.5	46	9	US-09-978-697-440	Sequence 440, App
C 879	12.6	13.5	25	10	US-09-827-998-1699	Sequence 1699, App	C 952	12.6	13.5	46	9	US-09-978-192A-440	Sequence 440, App
C 880	12.6	13.5	25	10	US-09-827-998-1700	Sequence 1700, App	C 953	12.6	13.5	46	9	US-09-978-824A-440	Sequence 440, App
C 881	12.6	13.5	25	10	US-09-827-998-1701	Sequence 1701, App	C 954	12.6	13.5	46	9	US-09-978-824A-440	Sequence 440, App
C 882	12.6	13.5	25	10	US-09-827-998-1702	Sequence 1702, App	C 955	12.6	13.5	46	9	US-09-978-824A-440	Sequence 440, App
C 883	12.6	13.5	25	10	US-09-906-453-8	Sequence 8, Appl	C 956	12.6	13.5	46	9	US-09-878-608A-440	Sequence 440, App
C 884	12.6	13.5	29	9	US-10-114-893-270	Sequence 270, App	C 957	12.6	13.5	46	9	US-09-878-191A-440	Sequence 440, App
C 885	12.6	13.5	29	9	US-09-948-977A-42	Sequence 42, App	C 958	12.6	13.5	46	9	US-09-978-564A-440	Sequence 440, App
C 886	12.6	13.5	29	9	US-10-235-056-20	Sequence 20, App	C 959	12.6	13.5	46	9	US-09-978-585A-440	Sequence 440, App
C 887	12.6	13.5	29	9	US-09-116-676-28	Sequence 28, App	C 960	12.6	13.5	46	9	US-10-017-081A-440	Sequence 440, App
C 888	12.6	13.5	29	9	US-10-016-249-46	Sequence 46, App	C 961	12.6	13.5	46	9	US-09-978-824A-440	Sequence 440, App
C 889	12.6	13.5	30	12	US-10-040-916-55	Sequence 55, App	C 962	12.6	13.5	46	9	US-09-981-951A-440	Sequence 440, App
C 890	12.6	13.5	30	10	US-10-005-338B-144	Sequence 144, App	C 963	12.6	13.5	46	9	US-09-899-833A-440	Sequence 440, App
C 891	12.6	13.5	30	10	US-09-748-451-18	Sequence 18, App	C 964	12.6	13.5	46	9	US-10-167-749-440	Sequence 440, App
C 892	12.6	13.5	31	9	US-09-778-900A-11	Sequence 11, Appl	C 965	12.6	13.5	46	9	US-09-918-585A-440	Sequence 440, App
C 893	12.6	13.5	31	9	US-10-007-527A-27	Sequence 27, Appl	C 966	12.6	13.5	46	9	US-09-978-433A-440	Sequence 440, App
C 894	12.6	13.5	31	9	US-09-895-940B-11	Sequence 11, Appl	C 967	12.6	13.5	46	9	US-10-013-921A-440	Sequence 440, App
C 895	12.6	13.5	31	9			C 968	12.6	13.5	46	9	US-09-978-133A-440	Sequence 440, App

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c 969 12.6 13.5 46 9 US-10-013-929A-440 Sequence 440, App
c 970 12.6 13.5 46 9 US-10-016-177A-440 Sequence 440, App
c 971 12.6 13.5 46 9 US-09-899-830A-440 Sequence 440, App
c 972 12.6 13.5 46 9 US-09-878-757A-440 Sequence 440, App
c 973 12.6 13.5 46 9 US-09-453-234-14 Sequence 14, Appl
c 974 12.6 13.5 46 9 US-09-978-187B-440 Sequence 440, App
c 975 12.6 13.5 46 9 US-09-978-643A-440 Sequence 440, App
c 976 12.6 13.5 46 10 US-10-166-709A-440 Sequence 440, App
c 977 12.6 13.5 46 10 US-09-875-945-10 Sequence 10, Appl
c 978 12.6 13.5 46 10 US-09-263-959-143 Sequence 143, App
c 979 12.6 13.5 48 9 US-09-892-598-385 Sequence 385, App
c 980 12.6 13.5 48 9 US-09-889-293A-385 Sequence 385, App
c 981 12.6 13.5 48 9 US-09-889-735-385 Sequence 385, App
c 982 12.6 13.5 48 9 US-09-990-444-385 Sequence 385, App
c 983 12.6 13.5 48 9 US-09-989-730-385 Sequence 385, App
c 984 12.6 13.5 48 9 US-09-990-436-385 Sequence 385, App
c 985 12.6 13.5 48 9 US-09-991-181-385 Sequence 385, App
c 986 12.6 13.5 48 9 US-09-993-687-385 Sequence 385, App
c 987 12.6 13.5 48 9 US-09-989-734-385 Sequence 385, App
c 988 12.6 13.5 48 9 US-09-997-653-385 Sequence 385, App
c 989 12.6 13.5 48 9 US-09-993-667-385 Sequence 385, App
c 990 12.6 13.5 48 9 US-09-999-724-14 Sequence 14, Appl
c 991 12.6 13.5 48 9 US-09-990-438-385 Sequence 385, App
c 992 12.6 13.5 48 9 US-09-990-562-385 Sequence 385, App
c 993 12.6 13.5 48 9 US-09-997-428-385 Sequence 385, App
c 994 12.6 13.5 48 9 US-09-997-666-385 Sequence 385, App
c 995 12.6 13.5 48 9 US-09-990-711-385 Sequence 385, App
c 996 12.6 13.5 48 9 US-09-989-726-385 Sequence 385, App
c 997 12.6 13.5 48 9 US-09-990-437-385 Sequence 385, App
c 998 12.6 13.5 48 9 US-09-988-156-385 Sequence 385, App
c 999 12.6 13.5 48 9 US-09-991-157-385 Sequence 385, App
c1000 12.6 13.5 48 9 US-09-991-172-385 Sequence 385, App
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ALIGNMENTS

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RESULT 1
; Sequence 22, Application US/09993170
; Patent No. US2002014804A1
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; FILE OF INVENTION: Specificity
; FILE REFERENCE: B1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Oligonucleotide
US-09-993-170-22
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Query Match 17.4%; Score 16.2; DB 10; Length 31;
Best Local Similarity 72.4%; Pred. No. 9.3e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 37 CCTGGTTTCAACACTATCGGATGTGAC 65
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Db 2 CCTGGATCCACACTAAGCTTATTATAC 30
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RESULT 2

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US-08-781-986A-2630/C
; Sequence 2630, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2630:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-2630
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Query Match 17.4%; Score 16.2; DB 7; Length 50;
Best Local Similarity 72.4%; Pred. No. 1.1e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 37 CCTGGTTTCAACACTATCGGATGTGAC 65
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Db 47 CCTGGTTTAAACCAATCGGCTTTTAC 19
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RESULT 3
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2
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Query Match	17.2%;	Score 16;	DB 9;	Length 43;
Best Local Similarity	79.2%;	Pred. No. 1.2e+04;		
Matches 19;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

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RESULT 4
US-09-801-371A-6/c
Sequence 6, Application US/09801371A
Patent No. US20020155569A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Jarrrous, Nayef
APPLICANT: Ben-Assouli, Yitshak
TITLE OF INVENTION: MANIPULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIORITY APPLICATION NUMBER: PCT WO 00/14255
PRIORITY FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 43
TYPE: DNA
ORGANISM: Homo sapien
US-09-801-371A-6

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RESULT 5
US-09-801-371A-8
Sequence 8. Application US/09801371A
Patent No. US20020155569A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF mRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-PCT-USA-A_060031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 50
TYPE: RNA
ORGANISM: Homo sapien
US-09-801-371A-8

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Db 11 UGGGGCCUCCAGAACTUCACUGGGG 34

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RESULT 6
US-10-098-263B-78554
; Sequence 78554, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098, 263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276, 759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ. ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1.1
; SEQ. ID NO 78554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-78554

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RESULT 7
US-10-158-735-10/c
: Sequence 10. Application US/10158735
: Publication No. US20020182744A1
: GENERAL INFORMATION:
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Friedrich, Glenn A.
: APPLICANT: Lilleberg, Stan
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: VECTORS FOR GENE MUTAGENESIS AND GENE
: TITLE OF INVENTION: DISCOVERY
: FILE REFERENCE: 7705-0006-01
: CURRENT APPLICATION NUMBER: US/10/158, 735
: CURRENT FILING DATE: 2002-05-29
: PRIOR APPLICATION NUMBER: US 09/276,533
: PRIOR FILING DATE: 1999-03-25
: PRIOR APPLICATION NUMBER: US 60/079,729
: PRIOR FILING DATE: 1998-03-27
: PRIOR APPLICATION NUMBER: US 60/081,727
: PRIOR FILING DATE: 1998-04-14
: PRIOR APPLICATION NUMBER: US 60/109,302
: PRIOR FILING DATE: 1998-11-20
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 39
: TYPE: DNA
: ORGANISM: Mus musculus
US-10-158-735-10

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QY      68 TCGGGCTCCAGAAACATTGAGG
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QY 15 CCATCTGCCTGGGTGACAAATG 36
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Db 22 CCGCTCGCCTGGATGACCAATG 1

RESULT 12

US-09-872-696A-40
; Sequence 40, Application US/09872696A
; Publication No. US20030104611A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Julie C.
; APPLICANT: Sauter, Sybille L.
; APPLICANT: Hsu, David
; APPLICANT: Sheridan, Phillip Lee
; APPLICANT: Hardy, Steven
; APPLICANT: Dubensky, Thomas
; APPLICANT: Yee, Jiling-Kuan
; TITLE OF INVENTION: FELINE IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
; FILE REFERENCE: 930049.467
; CURRENT APPLICATION NUMBER: US/09/872,696A
; PRIOR FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-872-696A-40

Query Match 16.3%; Score 15.2; DB 9; Length 46;
Best Local Similarity 66.7%; Pred. No. 2.6e+04;
Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 13 CTCATCTGCCTGGGTGACAAATGCGCTGG 42
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Db 13 CCGATCTACTCTGTGTGACTGTCCCTCGG 42

RESULT 13

US-09-231-235-40
; Sequence 40, Application US/09231235
; Patent No. US20020048805A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Julie C.
; APPLICANT: Sauter, Sybille L.
; APPLICANT: Hsu, David
; APPLICANT: Sheridan, Phillip Lee
; APPLICANT: Hardy, Steven
; APPLICANT: Dubensky, Thomas
; APPLICANT: Yee, Jiling-Kuan
; TITLE OF INVENTION: FELINE IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
; FILE REFERENCE: 930049.467
; CURRENT APPLICATION NUMBER: US/09/231,235
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; OTHER INFORMATION: Primer Used in Examples 5C and 5D
US-09-231-235-40

Query Match 16.3%; Score 15.2; DB 10; Length 46;
Best Local Similarity 66.7%; Pred. No. 2.6e+04;
Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 13 CTCATCTGCCTGGGTGACAAATGCGCTGG 42
| | | | | | | | | | | | | | | | | | | | | |
Db 13 CCGATCTACTCTGTGTGACTGTCCCTCGG 42

RESULT 14

US-09-797-518A-40
; Sequence 40, Application US/09797518A
; Patent No. US20020068354A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Julie C.
; APPLICANT: Sauter, Sybille L.
; APPLICANT: Hsu, David
; APPLICANT: Sheridan, Phillip Lee
; APPLICANT: Hardy, Steven
; APPLICANT: Dubensky, Thomas
; APPLICANT: Yee, Jiling-Kuan
; TITLE OF INVENTION: FELINE IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
; FILE REFERENCE: 930049.467
; CURRENT APPLICATION NUMBER: US/09/797,518A
; PRIOR FILING DATE: 2001-03-01
; CURRENT APPLICATION NUMBER: 09/231,235
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-797-518A-40

Query Match 16.3%; Score 15.2; DB 10; Length 46;
Best Local Similarity 66.7%; Pred. No. 2.6e+04;
Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 13 CTCATCTGCCTGGGTGACAAATGCGCTGG 42
| | | | | | | | | | | | | | | | | | | | | |
Db 13 CCGATCTACTCTGTGTGACTGTCCCTCGG 42

RESULT 15

US-09-935-280-15
; Sequence 15, Application US/09935280
; Publication No. US20030022179A1
; GENERAL INFORMATION:
; APPLICANT: INVITROGEN CORPORATION
; APPLICANT: CHESTNUT, John
; APPLICANT: SHUMAN, Stewart
; APPLICANT: HEYMAN, John
; APPLICANT: MADSEN, Knut
; APPLICANT: BENNETT, Rob
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MOLECULAR CLONING
; FILE REFERENCE: INVIT1300-1
; CURRENT APPLICATION NUMBER: US/09/935,280
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,563
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Annealing oligonucleotide
US-09-935-280-15

Query Match 16.1%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 CAACACTATCGGAAT 60
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DB 1 CAACACTATCGGAAT 15

RESULT 16

US-10-003-021-5
; Sequence 5, Application US/10003021
; Publication No. US20030073165A1
; GENERAL INFORMATION:
; APPLICANT: INVITROGEN CORPORATION
; APPLICANT: FERNANDEZ, Joseph
; APPLICANT: HEYMAN, John
; APPLICANT: HOEFFLER, James
; TITLE OF INVENTION: LIBRARIES OF EXPRESSIBLE GENE SEQUENCES
; FILE REFERENCE: INVIT1140-3
; CURRENT APPLICATION NUMBER: US/10/003,021
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/285,386
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: US 60/096,981
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: US 60/080,626
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Topo-5 oligonucleotide
US-10-003-021-5

Query Match 16.1%; Score 15; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 CAACACTATCGGAAT 60
|||||
DB 1 CAACACTATCGGAAT 15

RESULT 17

US-09-792-875-1
; Sequence 1, Application US/09792875
; Patent No. US20010044137A1
; GENERAL INFORMATION:
; APPLICANT: INVITROGEN CORPORATION
; APPLICANT: HEYMAN, John
; APPLICANT: STALAT, Gabot
; TITLE OF INVENTION: TOPOISOMERASE LINKER-MEDIATED AMPLIFICATION METHODS
; FILE REFERENCE: INVIT11270-1
; CURRENT APPLICATION NUMBER: US/09/792,875
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: oligonucleotide Topos
US-09-792-875-1

Query Match 16.1%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 CAACACTATCGGAAT 60
|||||

DB 1 CAACACTATCGGAAT 15

RESULT 18

US-10-098-263B-7295
; Sequence 7295, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 7295
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-7295

Query Match 16.1%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 2.5e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 GAGCACTCATCTCGCTGGGTG 30
|||||
DB 3 GAGCACTCATCTCGCTGGGTG 25

RESULT 19

US-10-098-263B-35881/C
; Sequence 35881, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35881
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35881

Query Match 16.1%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 AGAAAAATTCAGCT 92
|||||
DB 18 AGAAAAATTCAGCT 4

RESULT 20

US-10-098-263B-86605
; Sequence 86605, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86605
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-86605

Query Match 16.1%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 2.5e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 25 TGGGTGACATGCTTGGTTCA 47
|||||
DB 3 TGGGTGACATGCTTGGTTCA 25

RESULT 21

US-10-098-263B-116206/C
; Sequence 116206, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 116206
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-116206

Query Match 16.1%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 2.5e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 69 CGGAGCTCCAGAAACATGTAGG 91
|||||
DB 24 CGGAGCTCCGGAACACGAGC 2

RESULT 22

US-09-801-274-1732/C
; Sequence 1732, Application US/09801274
; Patent No. US2002003319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1732
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1732

Query Match 16.1%; Score 15; DB 10; Length 31;
Best Local Similarity 72.0%; Pred. No. 2.7e+04;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 28 GTGACATGCTTGGTTTCACACT 52
|||||
DB 28 GTGATGCTGCTTCCTTCACACT 4

RESULT 23

US-09-900-379-38
; Sequence 38, Application US/09900379
; Publication No. US20020198144A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Rhode, Peter R.
; APPLICANT: Widanz, Jon A.
; APPLICANT: Grammer, Susan
; APPLICANT: Edwards, Ana C.
; APPLICANT: Chavallaz, Pierre-Andre
; APPLICANT: Jiao, Jin-An
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/900,379
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,084
; FILING DATE: <unknown>
; APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-900-379-38

Query Match 16.1%; Score 15; DB 9; Length 42;
Best Local Similarity 67.7%; Pred. No. 3e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACCCATGCTGCGGAGTACATGCTG 41
|||||
DB 1 CCCCCAGGCTTCCCGGCGCACCATGCTG 31

RESULT 24
US-10-112-802-60/C
; Sequence 60, Application US/10112802

```
Publication No. US20030086942A1
GENERAL INFORMATION:
APPLICANT: Petersen, Jeannine M.
APPLICANT: Her, Lu-Shiun
APPLICANT: Dahlberg, James E.
APPLICANT: Glodowski, Doreen R.
TITLE OF INVENTION: Inhibition of Nucleocytoplasmic Transport by Vesicular
TITLE OF INVENTION: Stomatitis Virus M Protein-Like Polypeptides
FILE REFERENCE: 960296, 97770
CURRENT APPLICATION NUMBER: US/10/112,802
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 60/280,214
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 60
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-10-112-802-60

Query Match
Best Local Similarity 16.1%; Score 15; DB 9; Length 42;
Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GAGCTGGAGACATCTGCTGCTGGTGCATGCGCT 39
DB 42 GGGAGGGGCTTCCCATCTGCTGGCAATAAGCCCT 4

RESULT 25
US-10-112-802-61
Sequence 61, Application US/10112802
Publication No. US20030086942A1
GENERAL INFORMATION:
APPLICANT: Petersen, Jeannine M.
APPLICANT: Her, Lu-Shiun
APPLICANT: Dahlberg, James E.
APPLICANT: Glodowski, Doreen R.
TITLE OF INVENTION: Inhibition of Nucleocytoplasmic Transport by Vesicular
TITLE OF INVENTION: Stomatitis Virus M Protein-Like Polypeptides
FILE REFERENCE: 960296, 97770
CURRENT APPLICATION NUMBER: US/10/112,802
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 60/280,214
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 61
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-10-112-802-61

Query Match
Best Local Similarity 16.1%; Score 15; DB 9; Length 42;
Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GAGCTGGAGACATCTGCTGCTGGTGCATGCGCT 39
DB 1 GGGAGGGGCTTCCCATCTGCTGGCAATAAGCCCT 39

RESULT 26
US-09-848-164-38
Sequence 38, Application US/09848164
Patent No. US2002003451A1
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.

jiao, jin-an
Burkhardt, Martin
Wong, Hing
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dade International, Inc.
STREET: 1717 Deerfield Road
CITY: Deerfield
STATE: Illinois
COUNTRY: USA
ZIP: 60015
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/848,164
FILING DATE: 03-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,615
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-848-164-38

Query Match
Best Local Similarity 16.1%; Score 15; DB 10; Length 42;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCCATTCTGCTGCTGGTGCATGCGCTG 41
DB 1 CCCCCAGGCTTCCCGGCGCACCATGCGCTG 31

RESULT 27
US-10-156-306-7289
Sequence 7289, Application US/10156306
Publication No. US20030119017A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Moseygen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of IIR-gamma and PKR
FILE REFERENCE: MBRB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 7289
LENGTH: 48
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
```


US-10-156-306-7289

Query Match 16.1%; Score 15; DB 9; Length 48;
Best Local Similarity 47.8%; Pred. No. 3.1e+04;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 18 TTCTGCTGGGTGACATGCTT 40
:::||||| 11 11 11:
Db 1 UUCUGCCUGGAGGAACUCCCU 23

RESULT 28

US-10-098-263B-23348
; Sequence 23348, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098, 263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23348
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-23348

Query Match 15.9%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 62 TGACTGTCGGGCTCTCCAG 79
||||| 111111 111111
Db 7 TGACCGTGGGCTCTCCAG 24

RESULT 29

US-09-245-764-2
; Sequence 2, Application US/09245764
; Patent No. US20020107359A1
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maere S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Bpa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USUS THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/09/245, 764
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/099, 994
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/073, 972
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-09-245-764-2

Query Match 15.9%; Score 14.8; DB 10; Length 30;
Best Local Similarity 73.1%; Pred. No. 3.2e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 44 TTCAACACTATCGAATGTGACTGTC 69
||||| 111111 1111 11
Db 3 TTCTAGACTATGTGACACTGATGTC 28

RESULT 30

US-09-912-263-485/C
; Sequence 485, Application US/09912263
; Publication No. US20030039973A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825 2017-001
; CURRENT APPLICATION NUMBER: US/09/912, 263
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220, 315
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 552
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-912-263-485

Query Match 15.9%; Score 14.8; DB 9; Length 31;
Best Local Similarity 80.0%; Pred. No. 3.2e+04;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTGGAGACACTGCTATTCGC 23
||||| 111111 111111
Db 28 CTGGCTGCAATCATTCCTGC 9

RESULT 31

US-09-780-533A-3768
; Sequence 3768, Application US/09780533A
; Publication No. US2003006061A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowitra, Bharat
; APPLICANT: Haeblerl, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NGO Gene
; FILE REFERENCE: MBH90, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780, 533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3768
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for Inosine
US-09-780-533A-3768

Query Match 15.9%; Score 14.8; DB 9; Length 38;
Best Local Similarity 51.4%; Pred. No. 3.5e+04;
Matches 18; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 51 CTATCGAATGTGACTGTGGGCTCCAGAAACA 85
||:| 1111 1111 1111 1111
Db 4 CUAUCUGAUVGAGCGGCUUAGCGCCGAANCAACA 38

```
RESULT 32
US-10-043-573-147
; Sequence 147, Application US/10043573
; Publication No. US20030032025A1
; GENERAL INFORMATION:
; APPLICANT: Lemieux, Bertrand
; Landry, Benoit S.
; Sapolsky, Ronald J.
; TITLE OF INVENTION: Brassica polymorphisms
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS: 173
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/043,573
; FILING DATE: 09-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,507
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/032,069
; FILING DATE: 02-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-030100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 576-0200
; TELEFAX: 415 576-0200
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 147:
US-10-043-573-147

Query Match      15.9%; Score 14.8; DB 9; Length 41;
Best Local Similarity 61.1%; Pred. No. 3.5e+04;
Matches 22; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY      28 GTGCAATGCTGTTCAACACTGCGAATG 63
Db      6 GTGAAAGCATGTGCTCAAAATCTCGCTGCG 41

RESULT 33
US-10-060-275-7
; Sequence 7, Application US/10060275
; Publication No. US20030073828A1
; GENERAL INFORMATION:
; APPLICANT: DAT, ZIYU
; APPLICANT: SHI, LIFANG
; APPLICANT: HOOKER, BRIAN S.
; TITLE OF INVENTION: EPIMERASE GENE AND USE THEREOF
; FILE REFERENCE: 059440-0143
; CURRENT APPLICATION NUMBER: US/10/060,275
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/265,311
; PRIOR FILING DATE: 2001-02-01

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-060-275-7

Query Match      15.9%; Score 14.8; DB 9; Length 41;
Best Local Similarity 64.7%; Pred. No. 3.5e+04;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      59 ATGTGACTGTGCGGCTCCAGAAAACATTGAGGT 92
Db      8 ATATGGTGTTCAGTGTCAAGAAAATATTGCT 41

RESULT 34
US-09-904-380-12/c
; Sequence 12, Application US/09904380
; Patent No. US2002022229A1
; GENERAL INFORMATION:
; APPLICANT: Jane H. Morse and James A. Knowles
; TITLE OF INVENTION: Role of Pph1 Gene in Pulmonary Hypertension
; FILE REFERENCE: 0575/62430-A/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/904,380
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Human
US-09-904-380-12

Query Match      15.9%; Score 14.8; DB 10; Length 42;
Best Local Similarity 73.1%; Pred. No. 3.6e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      20 CTCCTGCGGTGCAATGCTTGGTT 45
Db      40 CTCCTGTAGACAAAGTATTACTTT 15

RESULT 35
US-10-076-631-4
; Sequence 4, Application US/10076631
; Publication No. US20030028001A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Use of supersecretable peptides in processes for their
; TITLE OF INVENTION: production and for parallel improvement of the exported
; TITLE OF INVENTION: forms of one or more other polypeptides of interest
; FILE REFERENCE: DEAY2001/0007
; CURRENT APPLICATION NUMBER: US/10/076,631
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hrfl
US-10-076-631-4

Query Match      15.9%; Score 14.8; DB 9; Length 46;
Best Local Similarity 64.7%; Pred. No. 3.7e+04;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      34 ATGCTTGTTCAACACTATGGAATGTGACTG 67
```


Best Local Similarity 62.2%; Pred. No. 4.3e+04;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 37 CCTGGTTCAACACTATCGAATGACTGCGGC 73
DB 39 CCGGGTTATCAATATCGGCGGCTGGTGGCC 3

RESULT 44

US-10-012-896-782
Sequence 782, Application US/10012896
Publication No. US20020183251A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 782
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-782

Query Match 15.7%; Score 14.6; DB 9; Length 45;
Best Local Similarity 57.8%; Pred. No. 4.4e+04;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 31 ACAATGCTTGGTTCAACACTATCGAATGACTGCGGCCT 75
DB 1 AGAATGCTTACCGTCTGCGAGTGGAGACGTGCGTGGTGTCT 45

RESULT 45

US-09-895-793-782
Sequence 782, Application US/09895793
Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 782
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-782

Query Match 15.7%; Score 14.6; DB 9; Length 45;
Best Local Similarity 57.8%; Pred. No. 4.4e+04;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 31 ACAATGCTTGGTTCAACACTATCGAATGACTGCGGCCT 75
DB 1 AGAATGCTTACCGTCTGCGAGTGGAGACGTGCGTGGTGTCT 45

RESULT 46

US-09-895-814-782
Sequence 782, Application US/09895814
Publication No. US20020193296A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 782
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens

US-09-895-814-782

Query Match	15.7%;	Score 14.6;	DB 9;	Length 45;
Best Local Similarity	57.8%;	Pred. No. 4.4e+04;		
Matches 26; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

```

QY      31 ACATGCCCTGGTTTCAACACTATCGGATGTGACTGTGGGGCT 75
          | | | | | | | | | | | | | | | | | | | |
Db      1 AGAATGCCCTACCGTGTGTCAGTGCCTGAACGTGTGGTGTCT 45

```

RESULT 47
US-09-759

; Sequence 782, Application US/09759143
; Patent No. US20020022248A1

```

? APPLICANT: Xu, Jiangchun
? APPLICANT: Dillon, Devin C.
? APPLICANT: Mitcham, Jennifer L.
? APPLICANT: Harlocker, Susan L.
? APPLICANT: Jiang, Yugu
? APPLICANT: Henderson, Robert A.
? APPLICANT: Kalos, Michael D.
? APPLICANT: Fanger, Gary R.
? APPLICANT: Retter, Marc W.
? APPLICANT: Stolk, John A.
? APPLICANT: Day, Craig H.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Darriack
? APPLICANT: Li, Samuel
? APPLICANT: Wang, Ajun
? APPLICANT:
? APPLICANT: Hepler, William
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C3
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 782
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-782

```

Query Match	15.7%	Score 14.6;	DB 10;	Length 45;
Best Local Similarity	57.8%;	Pred. No. 4.4e+04;		
Matches 26; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

```

QY      31 ACATGCCCTGGTTCAACACTATCGGAATGTACTGTGGGCGT 75
          | | | | | | | | | | | | | | | | | | | |
Db      1 AGATGCCCTACCGTCTGCAGTGCCTGACGTCGTCGTCGTC 45

```

RESULT 48
US-09-780-669-782

; Sequence 782, Application US/09780669
; Patent No. US20020051977A1

? APPLICANT: Xu, Jiangchun
 ? APPLICANT: Dillon, Davin C.
 ? APPLICANT: Mitcham, Jennifer L.
 ? APPLICANT: Harlockker, Susan L.
 ? APPLICANT: Jiang, Yugu
 ? APPLICANT: Henderson, Robert A.
 ? APPLICANT: Kalos, Michael D.
 ? APPLICANT: Ranger, Gary R.
 ? APPLICANT: Retzer, Marc W.
 ? APPLICANT: Stolk, John A.
 ? APPLICANT: Day, Craig H.
 ? APPLICANT: Vedvick, Thomas S.
 ? APPLICANT: Carter, Darick

```

APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasar A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghmon, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO: 782
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-782

```

Query Match	15.78;	Score 14.6;	DB 10;	Length 45;
Best Local Similarity	57.8%;	Pred. No. 4.4e+04;		
Matches 26;	Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0;

```

QY      31 ACAATGCCCTGGTTCAACACTATCGGAATGTACTGTGGGCT 75
      1 | | | | | | | | | | | | | | | | | |
Db      1 AGAATGCCCTACCGTGTCTGCAGTGCCTGAACGCTGTCGGTGTCT 45

```

RESULT 49
US-09-822-827-782

; Sequence 782, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:

```

? APPLICANT: Xu, Jianshun
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
? FILE REFERENCE: 210121.53401
? CURRENT APPLICATION NUMBER: US/09/822,827
? CURRENT FILING DATE: 2001-03-28
? NUMBER OF SEQ ID NOS: 982
? SOFTWARE: FastSeq for Version 3.0
? SEQ ID NO 782
? LENGTH: 45
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-822-827-782

```

Query Match	15.7%	Score 14.6;	DB 10;	Length 45;
Best Local Similarity	57.8%;	Pred. No. 4.4e+04;		
Matches 26; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

```

QY      31 ACAATGCGCTGGTTCAACACTATCGGAATGTACTGTGGGGCT 75
          | | | | | | | | | | | | | | | | | | | |
Db      1 AGAATGCGCTACCGTGTGCGAGTGCCTGAACGTCGTGGGTGCT 45

```

RESULT 50
US-09-918-063-53/

; Sequence 53, Application US/09918063
; Patent No. US20020098546A1

APPLICANT: Wedel, Eric R.
 APPLICANT: Jensen, Wayne A.
 APPLICANT: Chandrasekar, Ramaswamy
 TITLE OF INVENTION: CANINE TAG1 PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
 FILE REFERENCE: DI-12
 CURRENT APPLICATION NUMBER: US/09/918,063
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/224,655
 PRIOR FILING DATE: 2000-08-11
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: PatentIn version 3.1

SEQ ID NO 53
LENGTH: 45
TYPE: DNA
ORGANISM: Canis familiaris
NAME/KEY: CDS
LOCATION: (1)..(45)
OTHER INFORMATION:
US-09-918-063-53

Query Match
Best Local Similarity 57.8%; Score 14.6; DB 10; Length 45;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 4 CTGGGACACTCCATTCCTGCGGTGACAAATGCTTGGTTCAA 48
DB 45 CTGGGACCTCTCTCGGCAATGTGTTACAGAGCACTTGGTTCCA 1

RESULT 51
US-09-918-063-55

Sequence 55, Application US/09918063
Patent No. US20020098546A1
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
APPLICANT: Jensen, Wayne A.
APPLICANT: Chandrasekar, Ramaswamy
TITLE OF INVENTION: CANINE TRG1 PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: DI-12
CURRENT APPLICATION NUMBER: US/09/918,063
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/224,655
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 45
TYPE: DNA
ORGANISM: Canis familiaris
US-09-918-063-55

Query Match
Best Local Similarity 57.8%; Score 14.6; DB 10; Length 45;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 4 CTGGGACACTCCATTCCTGCGGTGACAAATGCTTGGTTCAA 48
DB 1 CTGGGACCTCTCTCGGCAATGTGTTACAGAGCACTTGGTTCCA 45

RESULT 52

US-09-996-073-19
Sequence 19, Application US/09996073
Publication No. US20030003565A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY JR., Thomas W.
APPLICANT: GASMI, Mehdi
APPLICANT: SAUTER, Sydille
TITLE OF INVENTION: FUNCTIONAL LENTIVIRAL VECTOR FROM
FILE REFERENCE: 2302-1642 / 1642.002
CURRENT APPLICATION NUMBER: US/09/996,073
CURRENT FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 46
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FIV9 primer
NAME/KEY: misc_feature

LOCATION: (29)
OTHER INFORMATION: "n" = "c" or "t"
US-09-996-073-19

Query Match
Best Local Similarity 66.7%; Score 14.6; DB 9; Length 46;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 13 CTCGATTCCTGCGGTGACAAATGCTTGG 42
DB 13 CCCATCTCTACTCTGTACTGTCCTCGG 42

RESULT 53

US-09-853-745-27/c
Sequence 27, Application US/09853745
Publication No. US20030039955A1
GENERAL INFORMATION:
APPLICANT: Feng, Yu
APPLICANT: Tang, Hengli
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION
FILE REFERENCE: 12934-002001
CURRENT APPLICATION NUMBER: US/09/853,745
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 60/206,997
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetically generated primer
US-09-853-745-27

Query Match
Best Local Similarity 62.2%; Score 14.6; DB 9; Length 48;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 16 CATTCGCTGCGGTGACAAATGCTTGGTTCAACACT 52
DB 48 CATTCGCTTGTGTACCCCTGCTTGTGCTCCTAATGT 12

RESULT 54

US-09-863-806-135
Sequence 135, Application US/09863806
Publication No. US20020197608A1
GENERAL INFORMATION:
APPLICANT: Sidransky, David
TITLE OF INVENTION: DETECTION OF NEOPLASIA BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,806
FILING DATE: 22-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/038,637
FILING DATE: <unknown>
APPLICATION NUMBER: 08/152,313

```

; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hallie, Lisa A.
;   REGISTRATION NUMBER: 38,347
;   REFERENCE/DOCKET NUMBER: 07265/146001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619/678-5070
;   TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 135:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 20 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-09-863-806-135

Query Match          15.5%; Score 14.4; DB 9; Length 20;
Best Local Similarity 93.8%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      22 GCCTGGGTGACATGC 37
Db      2 GCCTGGGTGACAAAC 17

RESULT 55
US-09-940-185-583/c
; Sequence 583, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
;   APPLICANT: Gunderson, Kevin
;   TITLE OF INVENTION: Probes and Decoder Oligonucleotides
;   FILE REFERENCE: A-69605-1
;   CURRENT APPLICATION NUMBER: US/09/940,185
;   CURRENT FILING DATE: 2001-08-27
;   PRIOR APPLICATION NUMBER: US 60/227,948
;   PRIOR FILING DATE: 2000-08-25
;   PRIOR APPLICATION NUMBER: US 60/228,854
;   PRIOR FILING DATE: 2000-08-29
;   NUMBER OF SEQ ID NOS: 4768
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 583
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-583

Query Match          15.5%; Score 14.4; DB 9; Length 24;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      38 CTGCTTCAACACTATCGAATG 61
Db      24 CTGATTTCAACTGCGCGGAATG 1

RESULT 56
US-10-215-112-2201
; Sequence 2201, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   TITLE OF INVENTION: Method of Genetic Analysis of Probes:
;   FILE REFERENCE: Test3
;   CURRENT APPLICATION NUMBER: US/10/215,112
;   CURRENT FILING DATE: 2002-08-08
;   NUMBER OF SEQ ID NOS: 14936
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2201
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2201

Query Match          15.5%; Score 14.4; DB 9; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      35 TGCCCTGGTTCAACACTATCGA 58
Db      2 TACCTGGTTTCGCCACTAAGCA 25

RESULT 57
US-10-215-112-13270/c
; Sequence 13270, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
;   APPLICANT: Michael Mittmann
;   TITLE OF INVENTION: Method of Genetic Analysis of Probes:
;   FILE REFERENCE: Test3
;   CURRENT APPLICATION NUMBER: US/10/215,112
;   CURRENT FILING DATE: 2002-08-08
;   NUMBER OF SEQ ID NOS: 14936
;   SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13270
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-13270

Query Match          15.5%; Score 14.4; DB 9; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      28 GTGACATGCTTGTTCAACAC 51
Db      24 GTATATGCTGCTAGTATCAACAC 1

RESULT 58
US-09-940-185-4551/c
; Sequence 4551, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
;   APPLICANT: Gunderson, Kevin
;   TITLE OF INVENTION: Probes and Decoder Oligonucleotides
;   FILE REFERENCE: A-69605-1
;   CURRENT APPLICATION NUMBER: US/09/940,185
;   CURRENT FILING DATE: 2001-08-27
;   PRIOR APPLICATION NUMBER: US 60/227,948
;   PRIOR FILING DATE: 2000-08-25
;   PRIOR APPLICATION NUMBER: US 60/228,854
;   PRIOR FILING DATE: 2000-08-29
;   NUMBER OF SEQ ID NOS: 4768
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4551
```


Query Match 15.5%; Score 14.4; DB 9; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 38 CTGGTTTCAACACTATGGAATG 61
DB 25 CTGGATTTCAACTCGCGGGAATG 2

RESULT 59

US-10-098-263B-97583
Sequence 97583, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 97583
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-263B-97583

Query Match 15.5%; Score 14.4; DB 9; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 63 GACTGTGCGGCTCCGAGAAACAT 86
DB 2 GACCCCTGAGACTCCAGAGACAT 25

RESULT 60

US-09-866-108-5065/C
Sequence 5065, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: A60MICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: A60MICA Sequence Listing Engine
SEQ ID NO 5065
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-5065

Query Match 15.5%; Score 14.4; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 23 CCGGGGACAAATGCGCTGTTTC 46
DB 25 CCAAGGCCCAATGCTGTGCTC 2

RESULT 61

US-09-866-108-5066/C
Sequence 5066, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: A60MICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860

PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acemica Sequence Listing Engine
SEQ ID NO 5066
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-5066

Query Match
Best Local Similarity 15.5%; Score 14.4; DB 10; Length 25;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 23 CCTGGTGACAAATGCTGTGTTTC 46
DB 24 CCAGGCGCACAAATGCTGTGTTTC 1

RESULT 62
US-09-126-816-2/c
Sequence 2, Application US/09126816
Publication No. US20030103987A1
GENERAL INFORMATION:
APPLICANT: BOEHRINGER MANNHEIM GMBH
TITLE OF INVENTION: METHOD OF INACTIVATION OF P21 RAS AND AGENTS THEREFOR
FILE REFERENCE: VON EICHEL-STREIBER
CURRENT FILING DATE: 1998-07-31
EARLIER FILING DATE: 1997-01-31
EARLIER APPLICATION NUMBER: PCT/EP97/00426
EARLIER FILING DATE: 1997-01-31
EARLIER APPLICATION NUMBER: 96 101 469.3
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer BCD2N
US-09-126-816-2

Query Match
Best Local Similarity 15.5%; Score 14.4; DB 9; Length 29;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 36 GCCTGGTTTCACACATATCGAA 59
DB 24 GACTGTGACTACATATATCGAA 1

RESULT 63
US-09-126-816-3
Sequence 3, Application US/09126816
Publication No. US20030103987A1
GENERAL INFORMATION:
APPLICANT: BOEHRINGER MANNHEIM GMBH
TITLE OF INVENTION: METHOD OF INACTIVATION OF P21 RAS AND AGENTS THEREFOR
FILE REFERENCE: VON EICHEL-STREIBER
CURRENT FILING DATE: 1998-07-31
EARLIER FILING DATE: 1997-01-31
EARLIER APPLICATION NUMBER: PCT/EP97/00426
EARLIER FILING DATE: 1997-01-31
EARLIER APPLICATION NUMBER: 96 101 469.3
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer BCD2C

US-09-126-816-3

Query Match
Best Local Similarity 15.5%; Score 14.4; DB 9; Length 29;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 36 GCCTGGTTTCACACATATCGAA 59
DB 6 GACTGTGACTACATATATCGAA 29

RESULT 64
US-08-837-459-10/c
Sequence 10, Application US/08837459
Patent No. US20020006407A1
GENERAL INFORMATION:
APPLICANT: McKee, Marian L.
APPLICANT: O'Brien, Allison D.
APPLICANT: Machiel, Marian R.
TITLE OF INVENTION: Histidine-tagged Inulin And Methods Of
TITLE OF INVENTION: Using Inulin To Stimulate An Immune Response And As An
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,459
FILING DATE: 18-Apr-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 04995.0023-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-837-459-10

Query Match
Best Local Similarity 15.5%; Score 14.4; DB 8; Length 34;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 36 GCCTGGTTTCACACATATCGAA 59
DB 25 GCCTGGTTTCACACATATCGAA 2

RESULT 65
US-10-017-178-10
Sequence 10, Application US/10017178
Patent No. US20020142287A1
GENERAL INFORMATION:
APPLICANT: Yamamoto, Hirotsuka
APPLICANT: Kosaki, Joseph R.
TITLE OF INVENTION: High Throughput Assay to Detect Inhibitors of the MAP Kinase P

FILE REFERENCE: 99.123-D
CURRENT APPLICATION NUMBER: US/10/017,178
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/255,548
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.1
SEQ ID NO 10
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-017-178-10

Query Match 15.5%; Score 14.4; DB 12; Length 35;
Best Local Similarity 75.0%; Pred. No. 4.8e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
DB 8 TCTTCTTATGACATGCTCTTG 31
19 TCTGCTGGGTGACATGCTTGG 42

RESULT 66
US-09-971-372A-30/C
Sequence 30, Application US/0971372A
Publication No. US20030035814A1
GENERAL INFORMATION:
APPLICANT: Kawaka, Yoshihiro
TITLE OF INVENTION: Recombinant Influenza viruses for vaccines and gene
FILE REFERENCE: 960296.98130
CURRENT APPLICATION NUMBER: US/09/971,372A
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: PCT/US00/090021
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/127,912
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 30
LENGTH: 46
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR primer
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(12)
OTHER INFORMATION: BsmBI recognition sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(46)
OTHER INFORMATION: Influenza virus sequence
US-09-971-372A-30

Query Match 15.5%; Score 14.4; DB 9; Length 46;
Best Local Similarity 65.6%; Pred. No. 5.2e+04;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
DB 46 CCATATGCTTGTGACCTGCTTGTCTCC 15
15 CCATTTGCTGCTGGTGACATGCTTGTTC 46
US-09-795-006A-35
Sequence 35, Application US/09795006A
Patent No. US20020151680A1
GENERAL INFORMATION:
APPLICANT: Alltalo et al

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
FILE REFERENCE: 28967/35977B
CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/205,331
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/185,205
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 35
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial chimeric
OTHER INFORMATION: oligonucleotide sequence derived from multiple vertebrate vasc
US-09-795-006A-35

Query Match 15.5%; Score 14.4; DB 10; Length 48;
Best Local Similarity 75.0%; Pred. No. 5.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
DB 10 GAAGGTGTTGTGCGACTCCAAA 33
57 GAATGAGCTGCGGCGCTCAGA 80

RESULT 68
US-10-078-337-26/C
Sequence 26, Application US/10078337
Publication No. US20030023068A1
GENERAL INFORMATION:
APPLICANT: YU, GUO-LIANG
DILLON, PATRICK J.
EBNER, REINHARD
ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/078,337
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,576
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0500001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
FAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-078-337-26

Query Match 15.5%: Score 14.4; DB 9; Length 49;
Best Local Similarity 60.0%; Pred. No. 5.4e+04;
Matches 24; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 53 ATCGAATGTGACTGCGGCTCCGAAACATTGAGGT 92
|| ||||| | | ||||| |||||
DB 41 ATAGAAATGTGCCCTCTTCTTCAATCAGAAAGCTTGGGT 2

RESULT 69
US-10-060-301-175/c
; Sequence 175, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1234-0195B
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-060-301-175

Query Match 15.3%: Score 14.2; DB 9; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 59 ATGTGACTGTGCGGCTCC 77
|| || ||||| |||||
DB 19 ATATGGCTGTGCGGCTCC 1

RESULT 70

US-09-864-636A-2543
; Sequence 2543, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:

; APPLICANT: Third Wave Technologies
; APPLICANT: Allwal, Hatim
; APPLICANT: Bartholomew, Christian
; APPLICANT: Chehak, Lukhne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2543
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-2543

Query Match 15.3%: Score 14.2; DB 9; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 GTGACTGTGCGGCTCCAG 79

DB 1 ||||| ||||| |||||
1 GGGACTGTGCGGACTTCAG 19

RESULT 71
US-10-098-263B-20064/c
; Sequence 20064, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20064
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-20064

Query Match 15.3%: Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 ACTATCGAATGTGACTGT 68
||| ||||| |||||
DB 19 ACTAAGGAATGTGAATGT 1

RESULT 72

US-10-098-263B-50784/c
; Sequence 50784, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-50784

Query Match 15.3%: Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 ACAATATCTGAATGTGAAT 66
|| ||||| |||||
DB 25 ACAATATCTGAATGTGAAT 7

RESULT 73

US-10-098-263B-78553
; Sequence 78553, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759

;; PRIOR FILING DATE: 2001-03-16
;; NUMBER OF SEQ ID NOS: 131066
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 78553
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-098-263B-78553

Query Match 15.3%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 66 TGTGGGCGCTCCAGAAAC 84
DB 2 TGTGGGCTCTCGAGAGAC 20

RESULT 74
US-09-801-274-54
; Sequence 54, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-54

Query Match 15.3%; Score 14.2; DB 10; Length 31;
Best Local Similarity 84.2%; Pred. No. 5.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 TGACTGTGGGCTCCAGA 80
DB 13 TGAAGTGGGCTCCAGA 31

RESULT 75
US-09-872-349-22/C
; Sequence 22, Application US/09872349
; Patent No. US20020132980A1
; GENERAL INFORMATION:
; APPLICANT: Sidney Pestka
; TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
; FILE REFERENCE: PBL-P01-007
; CURRENT APPLICATION NUMBER: US/09/872,349
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/208,240
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/255,296
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-872-349-22

Query Match 15.3%; Score 14.2; DB 10; Length 32;
Best Local Similarity 70.4%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCTGGAGACATCCATCTGCTGG 27
DB 32 GACCCAGACACATCCATCTGCTGG 6

RESULT 76
US-10-025-222A-18
; Sequence 18, Application US/10025222A
; Publication No. US20030003444A1
; GENERAL INFORMATION:
; APPLICANT: PELLETIER, JERRY
; APPLICANT: GROS, PHILIPPE
; APPLICANT: DUBOW, MICHAEL
; TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN
; FILE REFERENCE: 073406-0701
; CURRENT APPLICATION NUMBER: US/10/025,222A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,349
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-025-222A-18

Query Match 15.3%; Score 14.2; DB 9; Length 33;
Best Local Similarity 70.4%; Pred. No. 5.7e+04;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 34 ATGCTGTGGTTCAACACTTCGAAT 60
DB 6 ATCCCTACTATCAACACTTTCATAT 32

RESULT 77
US-09-829-124-5/C
; Sequence 5, Application US/09829124
; Patent No. US20020066122A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Swanson, Shane S.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM XANTHOMAS
; FILE REFERENCE: 21829/101
; CURRENT APPLICATION NUMBER: US/09/829,124
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/224,053
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/412,452
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/103,124
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 18 TTCGCGCTGGTGACAAAGCCT 39

Db 23 TTCGCGGAGTACAGCGCTCT 2

RESULT 81

US-09-940-185-1258

; Sequence 1258, Application US/09940185

; Publication No. US20030096239A1

; GENERAL INFORMATION:

; APPLICANT: Gunderson, Kevin

; TITLE OF INVENTION: Probes and Decoder Oligonucleotides

; FILE REFERENCE: A-69605-1

; CURRENT APPLICATION NUMBER: US/09/940,185

; PRIORITY FILING DATE: 2001-08-27

; PRIORITY FILING DATE: 2000-08-25

; PRIORITY FILING DATE: 2000-08-25

; PRIORITY FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 4768

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1258

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-1258

Query Match 15.1%; Score 14; DB 9; Length 24;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 66 TGTGGGCGCTCCAGAAACACT 87

Db 3 TGTGGGCGCTCCAGAAACACT 24

RESULT 82

US-10-215-112-919/c

; Sequence 919, Application US/10215112

; Publication No. US20030082596A1

; GENERAL INFORMATION:

; APPLICANT: Michael Miltman

; TITLE OF INVENTION: Method of Genetic Analysis of Probes:

; FILE REFERENCE: 3119

; CURRENT APPLICATION NUMBER: US/10/215,112

; PRIORITY FILING DATE: 2002-08-08

; PRIORITY FILING DATE: 2002-08-08

; PRIORITY FILING DATE: 2002-08-08

; NUMBER OF SEQ ID NOS: 14936

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 919

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-919

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 30 GACATGCGCTGGTGACAAAC 51

Db 22 GTCCATTCACAGGTTTCAACAC 1

RESULT 83

US-10-215-112-5487

; Sequence 5487, Application US/10215112

; Publication No. US20030082596A1

; GENERAL INFORMATION:

; APPLICANT: Michael Miltman

; TITLE OF INVENTION: Method of Genetic Analysis of Probes:

; FILE REFERENCE: 3119

; CURRENT APPLICATION NUMBER: US/10/215,112

; PRIORITY FILING DATE: 2002-08-08

; PRIORITY FILING DATE: 2002-08-08

; PRIORITY FILING DATE: 2002-08-08

; NUMBER OF SEQ ID NOS: 14936

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5487

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-5487

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 30 GACATGCGCTGGTGACAAAC 51

Db 4 GTCCATTCACAGGTTTCAACAC 25

RESULT 84

US-09-940-185-4487/c

; Sequence 4487, Application US/09940185

; Publication No. US20030096239A1

; GENERAL INFORMATION:

; APPLICANT: Gunderson, Kevin

; TITLE OF INVENTION: Probes and Decoder Oligonucleotides

; FILE REFERENCE: A-69605-1

; CURRENT APPLICATION NUMBER: US/09/940,185

; PRIORITY FILING DATE: 2001-08-27

; PRIORITY FILING DATE: 2000-08-25

; PRIORITY FILING DATE: 2000-08-25

; PRIORITY FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 4768

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4487

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-4487

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 18 TTCGCGCTGGTGACAAAGCCT 39

Db 24 TTCGCGGAGTACAGCGCTCT 3

RESULT 85

US-10-098-263B-62496

; Sequence 62496, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Miltman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; PRIORITY FILING DATE: 2003-01-08

; PRIORITY FILING DATE: 2003-01-08

; PRIORITY FILING DATE: 2003-01-08

PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 62496
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-62496

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 58 AATGTGACTGTGGGCTTCAG 79
||||| ||||| |||||
Db 1 AATGTGCTGTGCTTCTCCGC 22

RESULT 86
US-10-098-263B-76584
Sequence 76584, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 76584
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-76584

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 23 CCTGGTGCATGCTTGGT 44
||||| ||||| |||||
Db 2 CCTGGTTCATGTCAGGT 23

RESULT 87
US-10-098-263B-80753/C
Sequence 80753, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 80753
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-80753

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 55 CGGATGTGACTGTGGGCTTC 76
||||| ||||| |||||

Db 22 CGGATGCGACTTTCGACTTC 1

RESULT 88
US-10-098-263B-103164
Sequence 103164, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 103164
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-103164

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 28 GTGACATGCTTGGTTTCAAC 49
||||| ||||| |||||
Db 3 GTGATAGGTCATGCTTCAAC 24

RESULT 89
US-10-098-263B-112182
Sequence 112182, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 112182
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-112182

Query Match 15.1%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 6.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13 CTCGATCTGCTGGGTGACAA 34
||||| ||||| |||||
Db 1 CTCGATCTGCTGGGTGACAA 22

RESULT 90
US-10-097-672-3/C
Sequence 3, Application US/10097672
Publication No. US20030100759A1
GENERAL INFORMATION:
APPLICANT: Boston College
APPLICANT: Fraley, Andrew W
APPLICANT: McLaughlin, Larry W
APPLICANT: Dongli, Chen
APPLICANT: Lan, Tao
FILE REFERENCE: 2846/2012


```
;; CURRENT APPLICATION NUMBER: US/10/097,672
;; CURRENT FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: US 60/276,015
;; PRIOR FILING DATE: 2001-03-15
;; PRIOR APPLICATION NUMBER: US 60/317,026
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: US 60/337,854
;; PRIOR FILING DATE: 2001-12-05
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 3
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Human immunodeficiency virus
US-10-097-672-3
```

```
Query Match 15.1%; Score 14; DB 9; Length 30;
Best Local Similarity 66.7%; Pred. No. 6.6e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 26 GGGTGAACATGCTGCTTCAACACTATC 55
Db 30 GAGTGACATGCCATGATCCACAGATATAC 1
```

```
RESULT 91
US-09-903-456-103
;; Sequence 103, Application US/09903456
;; Patent No. US20020138874A1
;; GENERAL INFORMATION:
;; APPLICANT: Abbott Laboratories
;; APPLICANT: Mukerji, Pradip
;; APPLICANT: Leonard, Amanda Eun-Yeong
;; APPLICANT: Huang, Yung-Sheng
;; APPLICANT: Pereira, Suzette L.
;; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
;; FILE REFERENCE: 6407 US.P3
;; CURRENT APPLICATION NUMBER: US/09/903,456
;; CURRENT FILING DATE: 2001-07-11
;; PRIOR APPLICATION NUMBER: US 09/624,670
;; PRIOR FILING DATE: 2000-07-24
;; PRIOR APPLICATION NUMBER: US 09/379,095
;; PRIOR FILING DATE: 1999-08-23
;; PRIOR APPLICATION NUMBER: US 09/145,828
;; PRIOR FILING DATE: 1998-09-02
;; NUMBER OF SEQ ID NOS: 116
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 103
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer RO720
US-09-903-456-103
```

```
Query Match 15.1%; Score 14; DB 10; Length 30;
Best Local Similarity 66.7%; Pred. No. 6.6e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 27 GGTGACAATGCTGCTTCAACACTATC 56
Db 1 GGTTCACAGCTTGACTCAATCCTTCG 30
```

```
RESULT 92
US-09-912-263-506
;; Sequence 506, Application US/09912263
;; Publication No. US2003003973A1
;; GENERAL INFORMATION:
;; APPLICANT: Cargill, Michele
;; APPLICANT: Ireland, James S.
;; APPLICANT: Lander, Eric S.
;; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
```

```
;; FILE REFERENCE: 2825, 2017-001
;; CURRENT APPLICATION NUMBER: US/09/912,263
;; CURRENT FILING DATE: 2001-07-24
;; PRIOR APPLICATION NUMBER: US 60/220,315
;; PRIOR FILING DATE: 2000-07-24
;; NUMBER OF SEQ ID NOS: 552
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 506
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-912-263-506
```

```
Query Match 15.1%; Score 14; DB 9; Length 31;
Best Local Similarity 70.8%; Pred. No. 6.6e+04;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 13 CTCGATTCGCTGGGTGACATG 36
Db 2 CTAATTCCTCCGRTGGCATTTG 25
```

```
RESULT 93
US-10-029-314-20/c
;; Sequence 20, Application US/10029314
;; Publication No. US2003007701A1
;; GENERAL INFORMATION:
;; APPLICANT: Salton et al, John A.
;; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;; FILE REFERENCE: 1795/57453-C/JPW
;; CURRENT APPLICATION NUMBER: US/10/029,314
;; CURRENT FILING DATE: 2001-12-20
;; PRIOR APPLICATION NUMBER: 09/899,732
;; PRIOR FILING DATE: 2001-07-05
;; PRIOR APPLICATION NUMBER: 09/610,635
;; PRIOR FILING DATE: 2000-07-05
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 20
;; LENGTH: 32
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-10-029-314-20
```

```
Query Match 15.1%; Score 14; DB 9; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 11 CACTCCATTCGCTGGGTGACATGCTT 40
Db 30 CACTCCCTCTCTCGGCGCTCCCACTGACAT 1
```

```
RESULT 94
US-10-029-314-21
;; Sequence 21, Application US/10029314
;; Publication No. US2003007701A1
;; GENERAL INFORMATION:
;; APPLICANT: Salton et al, John A.
;; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
;; FILE REFERENCE: 1795/57453-C/JPW
;; CURRENT APPLICATION NUMBER: US/10/029,314
;; CURRENT FILING DATE: 2001-12-20
;; PRIOR APPLICATION NUMBER: 09/899,732
;; PRIOR FILING DATE: 2001-07-05
;; PRIOR APPLICATION NUMBER: 09/610,635
;; PRIOR FILING DATE: 2000-07-05
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn Ver. 2.1
```

SEQ ID NO: 21
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-10-029-314-21

Query Match 15.1%; Score 14; DB 9; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCCATTCTGCGGCGTGCACATGACCTT 40
DB 3 CACTCCCTTCTTCCGGCGCTCCACATGACAT 32

RESULT 95
US-09-899-732-20/c
Sequence 20, Application US/09899732
Publication No. US20030082623A1
GENERAL INFORMATION:
APPLICANT: Salton et al, John A.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
FILE REFERENCE: 1795/57453-C/JPW
CURRENT APPLICATION NUMBER: US/09/899,732
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/610,635
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-899-732-20

Query Match 15.1%; Score 14; DB 9; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCCATTCTGCGGCGTGCACATGACCTT 40
DB 30 CACTCCCTTCTTCCGGCGCTCCACATGACAT 1

RESULT 96
US-09-899-732-21
Sequence 21, Application US/09899732
Publication No. US20030082623A1
GENERAL INFORMATION:
APPLICANT: Salton et al, John A.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
FILE REFERENCE: 1795/57453-C/JPW
CURRENT APPLICATION NUMBER: US/09/899,732
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/610,635
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-899-732-21

Query Match 15.1%; Score 14; DB 9; Length 32;

Best Local Similarity 66.7%; Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCCATTCTGCGGCGTGCACATGACCTT 40
DB 3 CACTCCCTTCTTCCGGCGCTCCACATGACAT 32

RESULT 97
US-09-885-478-20/c
Sequence 20, Application US/09885478
Patent No. US20020111306A1
GENERAL INFORMATION:
APPLICANT: SALON, JOHN A
APPLICANT: LAZ, THOMAS M
APPLICANT: NAGORNY, RAISA
APPLICANT: WILSON, AMY E
TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
FILE REFERENCE: 1795/57453-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/885,478
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US99/31169
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 32
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: PRIMER
US-09-885-478-20

Query Match 15.1%; Score 14; DB 10; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACTCCATTCTGCGGCGTGCACATGACCTT 40
DB 30 CACTCCCTTCTTCCGGCGCTCCACATGACAT 1

RESULT 98
US-09-885-478-21
Sequence 21, Application US/09885478
Patent No. US20020111306A1
GENERAL INFORMATION:
APPLICANT: SALON, JOHN A
APPLICANT: LAZ, THOMAS M
APPLICANT: NAGORNY, RAISA
APPLICANT: WILSON, AMY E
TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (M
FILE REFERENCE: 1795/57453-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/885,478
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US99/31169
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 32
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: PRIMER
US-09-885-478-21

Query Match 15.1%; Score 14; DB 10; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Job time : 123 secs

QY 11 CACGCCATCTGCTGGTGACATGCTT 40
||||| ||||| ||||| |||||
Db 3 CACGCCATCTGCTGGTGACATGCTT 32

RESULT 99

US-10-102-949-2/c
; Sequence 2, Application US/10102949
; Patent No. US20020157140A1
; GENERAL INFORMATION:
; APPLICANT: Baono, Hirohara
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: ESRI - A PLANT GENE THAT CAN PROMOTE PLANT REGENERATION
; FILE REFERENCE: 2312-107-2
; CURRENT APPLICATION NUMBER: US/10/102,949
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/09/604,394
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Second strand
US-10-102-949-2

Query Match 15.1%; Score 14; DB 9; Length 34;
Best Local Similarity 66.7%; Pred. No. 6.8e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 10 GCACGCCATCTGCTGGTGACATGCTT 39
||| ||||| ||||| ||||| |||||
Db 30 GCACGCCATCTGCTGGTGACATGCTT 1

RESULT 100
US-10-005-956-1436/c
; Sequence 1436, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1436
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1436

Query Match 15.1%; Score 14; DB 9; Length 39;
Best Local Similarity 66.7%; Pred. No. 7.1e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 18 TTTCGCTGGTGACATGCTGGTTTCA 47
||||| ||||| ||||| ||||| |||||
Db 32 TTTCGCTGGTGACATGCTGGTTTCA 3

Search completed: July 5, 2003, 13:11:58

11

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 11:56:09 ; Search time 59 Seconds
(without alignments)
483.406 Million cell updates/sec

Title: US-09-843-377-3_COPY_1000_1092

Perfect score: 93

Sequence: 1 gagctggagagactcattc.....ctccagaaacattgagtg 93

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

609818

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2.6/ptodata/1/lna/5B.COMB.seq:*
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6: /cgn2.6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	20.0	45	2	US-08-602-716A-8
2	16.6	17.8	30	2	US-08-331-081B-14
3	16.6	17.8	39	1	US-08-225-224-31
4	16.6	17.8	39	3	US-08-722-258-31
5	16.6	17.8	39	5	PCT-US95-04468-31
6	16.6	17.8	49	1	US-08-198-670A-34
7	16.6	17.8	50	1	US-08-384-708A-5
8	16.6	17.8	50	4	US-08-687-421-5
9	16.4	17.6	47	4	US-08-957-001B-19
10	16.4	17.6	47	4	US-08-496-301-19
11	16.2	17.4	40	2	US-08-778-494B-103
12	15.8	17.0	39	4	US-09-276-533A-10
13	15.8	17.0	40	4	US-09-237-712-6
14	15.8	17.0	42	3	US-08-813-507-45
15	15.8	17.0	42	4	US-09-464-453-45
16	15.8	17.0	44	1	US-08-368-395-8
17	15.6	16.8	33	1	US-08-285-936-14
18	15.6	16.8	33	1	US-08-487-860-14
19	15.6	16.8	43	4	US-09-103-875-10
20	15.4	16.6	41	4	US-08-973-124-285
21	15.4	16.6	41	5	PCT-US96-08014-285
22	15.2	16.3	31	2	US-08-454-557C-63
23	15.2	16.3	31	2	US-08-340-426D-63
24	15.2	16.3	31	2	US-08-450-673C-63
25	15.2	16.3	36	4	PCT-US95-17111A-63
26	15.2	16.3	36	4	US-09-344-700-21
27	15.2	16.3	30	5	PCT-US94-14888-4
28	15.1	16.1	25	1	US-07-771-022F-8
29	15.1	16.1	32	2	US-08-596-319-7
30	15.1	16.1	33	1	US-07-771-022F-12
31	15.1	16.1	36	4	US-09-237-712-9
32	15.1	16.1	36	4	US-09-237-712-10
33	15.1	16.1	41	1	US-08-191-866D-91
34	15.1	16.1	41	3	US-08-480-640A-143
35	15.1	16.1	41	3	US-08-295-802-143
36	15.1	16.1	41	4	US-08-686-968C-70
37	15.1	16.1	41	4	US-08-488-237A-143
38	15.1	16.1	41	4	US-08-672-213-30
39	15.1	16.1	41	4	US-08-375-992A-143
40	15.1	16.1	42	2	US-08-596-387B-38
41	15.1	16.1	42	4	US-09-067-615-38
42	15.1	16.1	42	5	PCT-US95-09816A-38
43	15.1	16.1	45	1	US-08-681-935-13
44	15.1	16.1	45	4	US-08-939-323-13
45	14.8	15.9	27	4	US-08-584-040-3659
46	14.8	15.9	27	4	US-08-584-040-5068
47	14.8	15.9	30	2	US-08-332-562A-33
48	14.8	15.9	41	3	US-08-813-507-147
49	14.8	15.9	41	4	US-09-464-453-147
50	14.8	15.9	45	1	US-07-963-331D-5
51	14.6	15.7	25	4	US-09-167-681-6
52	14.6	15.7	25	4	US-09-167-681-12
53	14.6	15.7	31	2	US-08-557-128-23
54	14.6	15.7	33	3	US-08-564-109C-15
55	14.6	15.7	33	6	5504194-4
56	14.6	15.7	35	1	US-08-683-877-7
57	14.6	15.7	35	1	US-08-683-877-9
58	14.6	15.7	38	4	US-09-242-690A-30
59	14.6	15.7	40	1	US-08-431-080-9
60	14.6	15.7	40	2	US-08-185-949B-99
61	14.6	15.7	40	2	US-08-938-534-9
62	14.6	15.7	40	2	US-08-778-444B-100
63	14.6	15.7	40	4	US-08-483-511-80
64	14.6	15.7	40	4	US-09-345-294-9
65	14.6	15.7	43	3	US-08-832-985-74
66	14.6	15.7	43	4	US-09-410-903-55
67	14.6	15.7	45	1	US-08-229-279-4
68	14.6	15.7	45	1	US-08-701-269-4
69	14.6	15.7	45	4	US-09-605-785-782
70	14.6	15.7	47	2	US-08-184-009-187
71	14.6	15.7	47	2	US-08-458-356-187
72	14.6	15.7	47	4	US-08-460-736-187
73	14.6	15.7	48	1	US-08-093-453B-7
74	14.6	15.7	48	1	US-08-459-041A-4
75	14.6	15.7	48	1	US-08-459-041A-10
76	14.6	15.7	48	4	US-09-380-190A-36
77	14.4	15.5	20	4	US-09-038-657-135
78	14.4	15.5	32	1	US-07-613-083B-2
79	14.4	15.5	32	1	US-08-474-021-2
80	14.4	15.5	32	2	US-08-474-020A-2
81	14.4	15.5	32	5	PCT-US94-03426-2
82	14.4	15.5	34	4	US-08-840-466A-10
83	14.4	15.5	34	4	US-09-696-188B-10
84	14.4	15.5	39	4	US-09-375-318-6
85	14.4	15.5	40	1	US-08-301-722A-6
86	14.4	15.5	44	2	US-08-687-559-19
87	14.4	15.5	47	1	US-08-145-704A-44
88	14.4	15.5	47	3	US-08-987-574A-44
89	14.4	15.5	47	4	US-08-535-168-44
90	14.4	15.5	47	4	US-09-017-974-44
91	14.4	15.5	47	4	US-08-682-255A-44
92	14.4	15.5	47	4	US-09-429-130-44
93	14.4	15.5	47	5	PCT-US96-11786-44
94	14.4	15.5	49	4	US-08-916-576B-26
95	14.2	15.3	20	3	US-09-049-475-7
96	14.2	15.3	27	3	US-08-513-974B-81
97	14.2	15.3	28	1	US-08-340-011-16
98	14.2	15.3	28	1	US-08-901-710-16
99	14.2	15.3	29	2	US-08-331-081B-16
100	14.2	15.3	30	3	US-08-627-907A-8
					Sequence 8, Appl
					Sequence 7, Appl
					Sequence 12, Appl
					Sequence 9, Appl
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 12, Appl
					Sequence 13, Appl
					Sequence 14, Appl
					Sequence 15, Appl
					Sequence 16, Appl
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					Sequence 18, Appl
					Sequence 19, Appl
					Sequence 20, Appl
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 23, Appl
					Sequence 24, Appl
					Sequence 25, Appl
					Sequence 26, Appl
					Sequence 27, Appl
					Sequence 28, Appl
					Sequence 29, Appl
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					Sequence 93, Appl
					Sequence 94, Appl
					Sequence 95, Appl
					Sequence 96, Appl
					Sequence 97, Appl
					Sequence 98, Appl
					Sequence 99, Appl
					Sequence 100, Appl

C 101	14.2	15.3	35	2	US-08-331-081B-6	Sequence 6, Appl1	174	13.6	14.6	41	4	US-08-973-124-292	Sequence 292, App
C 102	14.2	15.3	36	1	US-08-153-799-12	Sequence 12, Appl1	175	13.6	14.6	41	5	PCT-US96-08014-292	Sequence 292, App
C 103	14.2	15.3	40	3	US-08-448-446B-16	Sequence 16, Appl	176	13.6	14.6	42	1	US-08-171-389-176	Sequence 176, App
C 104	14.2	15.3	42	3	US-08-813-507-131	Sequence 131, App	177	13.6	14.6	42	1	US-08-123-936-176	Sequence 176, App
C 105	14.2	15.3	42	4	US-09-464-453-131	Sequence 131, App	178	13.6	14.6	42	2	US-08-475-228A-176	Sequence 176, App
C 106	14.2	15.3	47	4	US-09-641-638-749	Sequence 749, App	179	13.6	14.6	42	3	US-08-483-080A-176	Sequence 176, App
C 107	14.2	15.1	27	3	US-08-776-251-8	Sequence 8, Appl1	180	13.6	14.6	42	4	US-09-354-947-176	Sequence 176, App
C 108	14.2	15.1	30	1	US-07-955-718-41	Sequence 41, Appl	181	13.6	14.6	42	5	PCT-US93-12388-176	Sequence 176, App
C 109	14.2	15.1	30	5	PCT-US91-05742-41	Sequence 41, Appl	182	13.6	14.6	43	2	US-08-613-235-8	Sequence 8, Appl1
C 110	14.2	15.1	33	1	US-08-134-570-6	Sequence 6, Appl1	183	13.6	14.6	45	1	US-08-176-412-5	Sequence 5, Appl1
C 111	14.2	15.1	33	1	US-08-134-570-6	Sequence 6, Appl1	184	13.6	14.6	45	2	US-08-555-268A-5	Sequence 5, Appl1
C 112	14.2	15.1	35	4	US-08-753-247-15	Sequence 15, Appl1	185	13.6	14.6	45	2	US-08-495-659B-5	Sequence 5, Appl1
C 113	14.2	15.1	36	1	US-08-653-740-39	Sequence 39, Appl	186	13.6	14.6	45	3	PCT-US94-1436-5	Sequence 5, Appl1
C 114	14.2	15.1	36	2	US-09-073-554-39	Sequence 39, Appl	187	13.6	14.6	47	4	US-09-641-638-956	Sequence 956, App
C 115	14.2	15.1	36	3	US-09-275-925-39	Sequence 39, Appl	188	13.6	14.6	48	2	US-08-841-178-12	Sequence 12, App
C 116	14.2	15.1	36	4	US-09-147-208-45	Sequence 45, Appl	189	13.6	14.6	48	4	US-09-461-697-288	Sequence 288, App
C 117	14.2	15.1	43	1	US-08-158-189-35	Sequence 35, Appl	190	13.6	14.6	50	1	US-08-753-054-6	Sequence 6, Appl1
C 118	14.2	15.1	43	1	US-08-343-682-16	Sequence 16, Appl	191	13.4	14.4	20	3	US-09-289-617-114	Sequence 114, App
C 119	14.2	15.1	43	1	US-08-483-389-81	Sequence 81, Appl	192	13.4	14.4	20	4	US-07-771-022E-10	Sequence 10, Appl
C 120	14.2	15.1	43	1	US-08-483-389-81	Sequence 81, Appl	193	13.4	14.4	25	1	US-07-705-490-9	Sequence 9, Appl1
C 121	14.2	15.1	43	2	US-08-487-113D-81	Sequence 81, Appl	194	13.4	14.4	25	3	US-07-751-891B-9	Sequence 9, Appl1
C 122	14.2	15.1	43	2	US-08-473-503-81	Sequence 81, Appl	195	13.4	14.4	25	4	US-07-751-891B-9	Sequence 9, Appl1
C 123	14.2	15.1	43	2	US-08-483-932-81	Sequence 81, Appl	196	13.4	14.4	26	2	US-08-210-762E-34	Sequence 34, Appl
C 124	14.2	15.1	43	2	US-08-720-420A-81	Sequence 81, Appl	197	13.4	14.4	26	4	US-09-106-075E-34	Sequence 34, Appl
C 125	14.2	15.1	43	3	US-08-714-017-81	Sequence 81, Appl	198	13.4	14.4	28	1	US-07-771-022E-13	Sequence 13, Appl
C 126	14.2	15.1	43	3	US-08-832-985-84	Sequence 84, Appl	199	13.4	14.4	28	1	US-08-484-557C-23	Sequence 23, Appl
C 127	14.2	15.1	43	3	US-08-475-680-81	Sequence 81, Appl	200	13.4	14.4	28	1	US-08-487-426E-23	Sequence 23, Appl
C 128	14.2	15.1	43	4	US-09-410-903-45	Sequence 45, Appl	201	13.4	14.4	28	2	US-08-487-720A-23	Sequence 23, Appl
C 129	14.2	15.1	45	2	US-08-700-670A-26	Sequence 26, Appl	202	13.4	14.4	28	2	US-08-859-998-490	Sequence 490, App
C 130	14.2	15.1	45	4	US-09-488-799-42	Sequence 42, Appl	203	13.4	14.4	28	4	US-09-225-628-490	Sequence 490, App
C 131	14.2	15.1	46	1	US-08-343-682-8	Sequence 8, Appl1	204	13.4	14.4	30	1	US-08-410-739-2	Sequence 2, Appl1
C 132	14.2	15.1	47	4	US-09-641-638-824	Sequence 824, Appl	205	13.4	14.4	30	1	US-08-697-815-2	Sequence 2, Appl1
C 133	14.2	15.1	48	1	US-08-158-189-41	Sequence 41, Appl	206	13.4	14.4	30	2	US-09-061-286-2	Sequence 2, Appl1
C 134	14.2	15.1	49	4	US-09-311-626B-60	Sequence 60, Appl	207	13.4	14.4	30	2	US-08-875-062-14	Sequence 14, Appl
C 135	14.2	15.1	50	1	US-08-477-254A-21	Sequence 21, Appl	208	13.4	14.4	31	1	US-08-314-615-7	Sequence 7, Appl1
C 136	14.2	15.1	50	2	US-08-472-576B-21	Sequence 21, Appl	209	13.4	14.4	31	1	US-08-314-362-7	Sequence 7, Appl1
C 137	14.2	15.1	50	2	US-08-428-734B-21	Sequence 21, Appl	210	13.4	14.4	31	1	US-08-433-010-7	Sequence 7, Appl1
C 138	14.2	15.1	50	4	US-08-713-556F-21	Sequence 21, Appl	211	13.4	14.4	31	1	US-08-483-882-7	Sequence 7, Appl1
C 139	13.8	14.8	20	4	US-09-851-520-40	Sequence 40, Appl	212	13.4	14.4	31	1	US-08-483-389-7	Sequence 7, Appl1
C 140	13.8	14.8	21	1	US-08-137-252-4	Sequence 4, Appl1	213	13.4	14.4	31	2	US-08-487-1130-7	Sequence 7, Appl1
C 141	13.8	14.8	30	2	US-09-038-227-41	Sequence 41, Appl	214	13.4	14.4	31	2	US-08-473-503-7	Sequence 7, Appl1
C 142	13.8	14.8	30	4	US-07-861-458C-35	Sequence 35, Appl	215	13.4	14.4	31	2	US-08-483-932-7	Sequence 7, Appl1
C 143	13.8	14.8	33	2	US-08-942-423-46	Sequence 46, Appl	216	13.4	14.4	31	2	US-08-942-423-53	Sequence 53, Appl1
C 144	13.8	14.8	33	4	US-09-116-032-14	Sequence 14, Appl	217	13.4	14.4	31	2	US-08-720-420A-7	Sequence 7, Appl1
C 145	13.8	14.8	36	3	US-08-888-949-13	Sequence 13, Appl	218	13.4	14.4	31	3	US-08-714-017-7	Sequence 7, Appl1
C 146	13.8	14.8	36	4	US-08-888-950-13	Sequence 13, Appl	219	13.4	14.4	31	3	US-08-863-790-7	Sequence 7, Appl1
C 147	13.8	14.8	36	4	US-09-262-758-13	Sequence 13, Appl	220	13.4	14.4	31	3	US-08-475-680-7	Sequence 7, Appl1
C 148	13.8	14.8	41	1	US-08-211-202-89	Sequence 89, Appl	221	13.4	14.4	31	3	US-08-296-749-7	Sequence 7, Appl1
C 149	13.8	14.8	46	1	US-08-171-389-135	Sequence 135, App	222	13.4	14.4	33	3	US-08-564-109C-14	Sequence 14, Appl
C 150	13.8	14.8	46	1	US-08-123-936-135	Sequence 135, App	223	13.4	14.4	34	1	US-08-443-965B-7	Sequence 7, Appl1
C 151	13.8	14.8	46	2	US-08-475-228A-135	Sequence 135, App	224	13.4	14.4	34	2	US-08-425-989B-7	Sequence 7, Appl1
C 152	13.8	14.8	46	3	US-08-482-080A-135	Sequence 135, App	225	13.4	14.4	34	2	US-08-443-966B-7	Sequence 7, Appl1
C 153	13.8	14.8	46	4	US-09-354-947-135	Sequence 135, App	226	13.4	14.4	34	3	US-09-142-759-29	Sequence 29, Appl
C 154	13.8	14.8	46	5	PCT-US93-12388-135	Sequence 135, App	227	13.4	14.4	35	3	US-08-952-948-2	Sequence 2, Appl1
C 155	13.8	14.8	50	1	US-08-449-045C-25	Sequence 25, Appl	228	13.4	14.4	38	1	US-08-541-632-1	Sequence 1, Appl1
C 156	13.8	14.8	50	1	US-08-449-045C-26	Sequence 26, Appl	229	13.4	14.4	38	1	US-09-325-554-16	Sequence 16, Appl
C 157	13.8	14.8	50	2	US-08-433-605A-37	Sequence 37, Appl	230	13.4	14.4	39	4	US-08-220-606B-20	Sequence 20, Appl
C 158	13.8	14.8	50	2	US-08-435-605A-38	Sequence 38, Appl	231	13.4	14.4	40	1	US-08-199-507B-48	Sequence 48, Appl
C 159	13.8	14.6	20	4	US-09-315-794-9	Sequence 9, Appl1	232	13.4	14.4	40	1	US-08-199-507B-48	Sequence 48, Appl
C 160	13.6	14.6	20	4	US-09-389-341-9	Sequence 9, Appl1	233	13.4	14.4	40	1	US-08-441-828-30	Sequence 30, Appl
C 161	13.6	14.6	20	4	US-09-315-793-9	Sequence 9, Appl1	234	13.4	14.4	40	1	US-08-441-828-30	Sequence 48, Appl
C 162	13.6	14.6	20	4	US-09-313-932-668	Sequence 468, App	235	13.4	14.4	40	4	US-09-198-603C-13	Sequence 13, Appl
C 163	13.6	14.6	32	4	US-09-052-919-60	Sequence 60, Appl	236	13.4	14.4	41	1	US-08-702-795-1	Sequence 1, Appl1
C 164	13.6	14.6	32	2	US-08-596-319-6	Sequence 6, Appl1	237	13.4	14.4	42	1	US-08-073-384C-19	Sequence 19, Appl
C 165	13.6	14.6	34	1	US-08-417-330A-3	Sequence 3, Appl1	238	13.4	14.4	42	1	US-08-254-559A-19	Sequence 19, Appl
C 166	13.6	14.6	36	1	US-08-173-510B-53	Sequence 53, Appl	239	13.4	14.4	42	1	US-08-225-224-28	Sequence 28, Appl
C 167	13.6	14.6	36	1	US-08-458-218-53	Sequence 53, Appl	240	13.4	14.4	42	1	US-08-483-043-19	Sequence 19, Appl
C 168	13.6	14.6	36	2	US-08-450-497-53	Sequence 53, Appl	241	13.4	14.4	42	1	US-08-481-238-19	Sequence 19, Appl
C 169	13.6	14.6	36	4	US-09-315-127-19	Sequence 19, Appl	242	13.4	14.4	42	2	US-08-471-066B-19	Sequence 19, Appl
C 170	13.6	14.6	39	3	US-08-975-703-37	Sequence 37, Appl	243	13.4	14.4	42	2	US-08-484-956-19	Sequence 19, Appl
C 171	13.6	14.6	39	4	US-09-515-884-37	Sequence 37, Appl	244	13.4	14.4	42	2	US-08-757-653-19	Sequence 19, Appl
C 172	13.6	14.6	40	5	PCT-US94-08052-9	Sequence 9, Appl1	245	13.4	14.4	42	2	US-08-599-91-19	Sequence 19, Appl
C 173	13.6	14.6	41	1	US-08-399-696-40	Sequence 40, Appl1	246	13.4	14.4	42	2	US-08-756-386-19	Sequence 19, Appl

C 247	13.4	14.4	42	2	US-08-823-516-19	Sequence 19, Appl	C 320	13.2	14.2	46	5	PCT-US94-05085-8	Sequence 8, Appl
C 248	13.4	14.4	42	3	US-08-862-853A-19	Sequence 19, Appl	C 321	13.2	14.2	47	3	US-08-646-538-12	Sequence 12, Appl
C 249	13.4	14.4	42	3	US-08-722-258-28	Sequence 28, Appl	C 322	13.2	14.2	47	3	US-08-864-473-63	Sequence 63, Appl
C 250	13.4	14.4	42	3	US-08-759-038-19	Sequence 19, Appl	C 323	13.2	14.2	47	4	US-09-338-907-309	Sequence 309, Appl
C 251	13.4	14.4	42	3	US-08-758-314-19	Sequence 19, Appl	C 324	13.2	14.2	47	4	US-09-338-907-309	Sequence 309, Appl
C 252	13.4	14.4	42	4	US-09-350-309-19	Sequence 19, Appl	C 325	13.2	14.2	47	4	US-09-503-222-12	Sequence 12, Appl
C 253	13.4	14.4	42	4	US-08-520-946-19	Sequence 19, Appl	C 326	13.2	14.2	47	4	US-09-440-523-63	Sequence 63, Appl
C 254	13.4	14.4	42	4	PCT-US95-04468-8	Sequence 21, Appl	C 327	13.2	14.2	47	4	US-09-489-979-1	Sequence 1, Appl
C 255	13.4	14.4	44	2	US-08-761-277A-11	Sequence 71, Appl	C 328	13.2	14.2	47	4	US-09-218-207-232	Sequence 232, Appl
C 256	13.4	14.4	46	4	US-09-198-955A-12	Sequence 12, Appl	C 329	13.2	14.2	47	4	US-09-218-207-232	Sequence 232, Appl
C 257	13.4	14.4	46	4	US-08-862-124-12	Sequence 12, Appl	C 330	13.2	14.2	47	4	US-09-641-638-1260	Sequence 1260, Appl
C 258	13.4	14.4	46	4	US-08-872-056-19	Sequence 19, Appl	C 331	13.2	14.2	48	1	US-08-176-412-12	Sequence 12, Appl
C 259	13.4	14.4	46	4	US-08-694-531-29	Sequence 29, Appl	C 332	13.2	14.2	48	1	US-08-190-199A-54	Sequence 54, Appl
C 260	13.4	14.4	47	1	US-08-482-882-102	Sequence 102, Appl	C 333	13.2	14.2	48	2	US-08-555-268A-12	Sequence 12, Appl
C 261	13.4	14.4	47	1	US-08-483-389-102	Sequence 102, Appl	C 334	13.2	14.2	48	2	US-08-495-695B-12	Sequence 12, Appl
C 262	13.4	14.4	47	2	US-08-487-111D-102	Sequence 102, Appl	C 335	13.2	14.2	48	3	US-08-864-473-1	Sequence 1, Appl
C 263	13.4	14.4	47	2	US-08-473-503-102	Sequence 102, Appl	C 336	13.2	14.2	48	4	US-09-440-523-1	Sequence 1, Appl
C 264	13.4	14.4	47	2	US-08-483-932-102	Sequence 102, Appl	C 337	13.2	14.2	48	5	PCT-US94-14436-12	Sequence 12, Appl
C 265	13.4	14.4	47	2	US-08-720-420A-102	Sequence 102, Appl	C 338	13.2	14.0	23	4	US-09-522-217-103	Sequence 103, Appl
C 266	13.4	14.4	47	3	US-08-714-017-102	Sequence 102, Appl	C 339	13.2	14.0	25	1	US-08-243-544-9	Sequence 9, Appl
C 267	13.4	14.4	47	3	US-08-475-680-102	Sequence 102, Appl	C 340	13.2	14.0	25	1	US-08-374-144-5	Sequence 5, Appl
C 268	13.4	14.4	47	4	US-09-641-638-930	Sequence 930, Appl	C 341	13.2	14.0	25	1	US-08-775-164-5	Sequence 5, Appl
C 269	13.4	14.4	47	4	US-09-641-638-969	Sequence 969, Appl	C 342	13.2	14.0	25	2	US-08-775-609-5	Sequence 5, Appl
C 270	13.4	14.4	48	4	US-08-691-271-29	Sequence 29, Appl	C 343	13.2	14.0	25	2	US-08-775-609-5	Sequence 5, Appl
C 271	13.4	14.4	48	4	US-08-691-271-29	Sequence 29, Appl	C 344	13.2	14.0	25	2	PCT-US93-06828-5	Sequence 5, Appl
C 272	13.4	14.4	50	6	5508178-3	Patent No. 5508178	C 345	13.2	14.0	28	4	US-09-150-900-26	Sequence 26, Appl
C 273	13.2	14.2	18	2	US-08-691-814B-58	Sequence 58, Appl	C 346	13.2	14.0	29	1	US-08-484-686B-46	Sequence 46, Appl
C 274	13.2	14.2	20	1	US-08-171-718-70	Sequence 70, Appl	C 347	13.2	14.0	29	4	US-08-463-160B-46	Sequence 46, Appl
C 275	13.2	14.2	20	3	US-08-289-267-165	Sequence 165, Appl	C 348	13.2	14.0	29	4	US-09-574-432-5	Sequence 5, Appl
C 276	13.2	14.2	20	3	US-08-478-087-70	Sequence 70, Appl	C 349	13.2	14.0	30	1	US-08-196-538-10	Sequence 10, Appl
C 277	13.2	14.2	20	4	US-09-313-932-354	Sequence 354, Appl	C 350	13.2	14.0	31	1	US-07-971-819A-43	Sequence 43, Appl
C 278	13.2	14.2	20	5	PCT-US95-04138-1	Sequence 1, Appl	C 351	13.2	14.0	31	1	US-08-475-231-43	Sequence 43, Appl
C 279	13.2	14.2	21	4	US-09-479-128-19	Sequence 19, Appl	C 352	13.2	14.0	31	1	US-08-220-606B-5	Sequence 5, Appl
C 280	13.2	14.2	21	4	US-09-233-086-61	Sequence 61, Appl	C 353	13.2	14.0	31	1	US-08-147-696E-18	Sequence 18, Appl
C 281	13.2	14.2	26	2	US-08-859-998-513	Sequence 513, Appl	C 354	13.2	14.0	31	1	US-08-484-334-18	Sequence 18, Appl
C 282	13.2	14.2	26	4	US-09-325-928-513	Sequence 513, Appl	C 355	13.2	14.0	31	2	US-08-583-536B-13	Sequence 13, Appl
C 283	13.2	14.2	27	2	US-08-859-998-1252	Sequence 1252, Appl	C 356	13.2	14.0	31	2	US-08-859-998-138	Sequence 138, Appl
C 284	13.2	14.2	27	4	US-08-225-928-1252	Sequence 1252, Appl	C 357	13.2	14.0	31	3	US-09-013-092-18	Sequence 18, Appl
C 285	13.2	14.2	28	2	US-08-743-637B-99	Sequence 99, Appl	C 358	13.2	14.0	31	3	US-09-280-999-18	Sequence 18, Appl
C 286	13.2	14.2	28	3	US-08-926-840B-99	Sequence 99, Appl	C 359	13.2	14.0	31	4	US-09-225-928-138	Sequence 138, Appl
C 287	13.2	14.2	30	2	US-08-942-423-45	Sequence 45, Appl	C 360	13.2	14.0	32	4	US-08-653-648A-40	Sequence 40, Appl
C 288	13.2	14.2	30	4	US-08-218-369-11	Sequence 11, Appl	C 361	13.2	14.0	33	1	US-08-431-080-13	Sequence 13, Appl
C 289	13.2	14.2	30	4	US-09-364-539-149	Sequence 149, Appl	C 362	13.2	14.0	33	2	US-08-938-584-13	Sequence 52, Appl
C 290	13.2	14.2	30	5	PCT-US95-03742-11	Sequence 11, Appl	C 363	13.2	14.0	33	4	US-09-039-982A-52	Sequence 52, Appl
C 291	13.2	14.2	31	2	US-08-418-085-19	Sequence 19, Appl	C 364	13.2	14.0	33	4	US-09-214-278-32	Sequence 32, Appl
C 292	13.2	14.2	31	4	US-09-099-011A-19	Sequence 19, Appl	C 365	13.2	14.0	33	4	US-09-068-740A-24	Sequence 24, Appl
C 293	13.2	14.2	31	4	US-09-495-797-12	Sequence 12, Appl	C 366	13.2	14.0	33	4	US-09-194-285-42	Sequence 42, Appl
C 294	13.2	14.2	31	6	5185441-7	Patent No. 5185441	C 367	13.2	14.0	33	4	US-09-042-294-13	Sequence 13, Appl
C 295	13.2	14.2	33	1	US-08-122-546-9	Sequence 9, Appl	C 368	13.2	14.0	33	4	US-09-345-294-13	Sequence 13, Appl
C 296	13.2	14.2	33	2	US-08-764-938-9	Sequence 9, Appl	C 369	13.2	14.0	33	4	US-08-913-612A-58	Sequence 58, Appl
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C 298	13.2	14.2	33	3	US-09-131-052-9	Sequence 9, Appl	C 371	13.2	14.0	34	1	US-08-478-940-2	Sequence 2, Appl
C 299	13.2	14.2	33	3	US-09-131-053A-9	Sequence 9, Appl	C 372	13.2	14.0	34	1	US-08-487-748A-22	Sequence 22, Appl
C 300	13.2	14.2	33	4	US-08-987-032-1	Sequence 1, Appl	C 373	13.2	14.0	35	1	US-08-480-070C-22	Sequence 22, Appl
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C 303	13.2	14.2	34	1	US-08-435-628-26	Sequence 26, Appl	C 376	13.2	14.0	35	4	US-08-468-413-5	Sequence 5, Appl
C 304	13.2	14.2	35	1	US-08-475-867A-15	Sequence 15, Appl	C 377	13.2	14.0	36	2	US-09-332-337-25	Sequence 25, Appl
C 305	13.2	14.2	35	1	US-08-477-883A-15	Sequence 15, Appl	C 378	13.2	14.0	37	4	US-09-310-367-25	Sequence 25, Appl
C 306	13.2	14.2	35	1	US-08-336-526A-15	Sequence 15, Appl	C 379	13.2	14.0	37	4	US-08-373-124A-1121	Sequence 1121, Appl
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C 308	13.2	14.2	35	1	US-08-478-940-14	Sequence 14, Appl	C 381	13.2	14.0	38	1	US-08-435-628-1121	Sequence 1121, Appl
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C 310	13.2	14.2	35	1	US-09-068-880-15	Sequence 15, Appl	C 383	13.2	14.0	38	1	US-08-316-439A-25	Sequence 25, Appl
C 311	13.2	14.2	38	4	US-09-387-800-6	Sequence 6, Appl	C 384	13.2	14.0	38	1	US-08-750-810-5	Sequence 5, Appl
C 312	13.2	14.2	38	4	US-09-308-160B-5	Sequence 5, Appl	C 385	13.2	14.0	38	1		
C 313	13.2	14.2	38	4	US-09-456-399-5	Sequence 5, Appl	C 386	13.2	14.0	38	1		
C 314	13.2	14.2	39	2	US-08-910-731-14	Sequence 14, Appl	C 387	13.2	14.0	38	1		
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C 317	13.2	14.2	43	2	US-08-418-085-17	Sequence 17, Appl	C 390	13.2	14.0	38	1		
C 318	13.2	14.2	43	4	US-09-099-011A-17	Sequence 17, Appl	C 391	13.2	14.0	38	1		
C 319	13.2	14.2	46	5	PCT-US94-05085A-8	Sequence 8, Appl	C 392	13.2	14.0	39	2		

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C 394	13	14.0	40	2	US-08-778-494B-90	Sequence 90, Appl	467	12.8	13.8	27	1	US-08-435-241A-18	Sequence 18, Appl
C 395	13	14.0	40	3	US-09-136-60B-18	Sequence 18, Appl	C 468	12.8	13.8	28	1	US-08-468-763-9	Sequence 5, Appl
C 396	13	14.0	40	4	US-08-483-511-81	Sequence 81, Appl	C 469	12.8	13.8	29	2	US-08-393-996A-5	Sequence 5, Appl
C 397	13	14.0	40	4	US-09-313-221A-95	Sequence 8, Appl	C 470	12.8	13.8	29	4	US-09-182-728A-3	Sequence 3, Appl
398	13	14.0	41	4	US-09-350-982C-8	Sequence 8, Appl	C 471	12.8	13.8	29	4	US-09-795-232-3	Sequence 3, Appl
C 400	13	14.0	42	4	US-09-502-653-23	Sequence 23, Appl	C 472	12.8	13.8	30	2	US-08-327-832-9	Sequence 9, Appl
C 401	13	14.0	43	2	US-08-881-687-13	Sequence 13, Appl	C 473	12.8	13.8	30	2	US-08-828-584-9	Sequence 9, Appl
C 402	13	14.0	43	3	US-08-832-985-80	Sequence 80, Appl	C 474	12.8	13.8	31	3	US-08-961-083-123	Sequence 323, App
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C 406	13	14.0	44	5	PCT-US95-09816A-40	Sequence 40, Appl	C 478	12.8	13.8	33	1	US-08-485-618-8	Sequence 87, Appl
C 407	13	14.0	45	1	US-08-038-768A-5	Sequence 5, Appl	C 479	12.8	13.8	33	1	US-07-813-338A-29	Sequence 29, Appl
C 408	13	14.0	45	1	US-08-229-279-3	Sequence 3, Appl	C 480	12.8	13.8	33	1	US-08-665-652-87	Sequence 87, Appl
C 409	13	14.0	45	1	US-08-701-269-3	Sequence 3, Appl	C 481	12.8	13.8	33	1	US-08-605-672-87	Sequence 87, Appl
C 410	13	14.0	45	6	5258287-9	Patent No. 5258287	C 482	12.8	13.8	33	2	US-08-482-283A-87	Sequence 87, Appl
C 411	13	14.0	47	4	US-09-402-631A-8	Sequence 8, Appl	C 483	12.8	13.8	33	2	US-08-943-363-87	Sequence 87, Appl
C 412	13	14.0	48	1	US-08-182-612B-8	Sequence 8, Appl	C 484	12.8	13.8	33	2	US-08-378-617A-15	Sequence 15, Appl
C 413	13	14.0	48	1	US-08-604-913B-7	Sequence 7, Appl	C 485	12.8	13.8	33	2	US-09-066-075-4	Sequence 4, Appl
C 414	13	14.0	48	1	US-08-604-913B-9	Sequence 9, Appl	C 486	12.8	13.8	33	2	US-08-636-602A-1	Sequence 1, Appl
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C 416	13	14.0	48	2	US-08-050-478-39	Sequence 39, Appl	C 488	12.8	13.8	33	2	US-08-636-602A-12	Sequence 12, Appl
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C 421	13	14.0	48	4	US-09-110-200-70	Sequence 70, Appl	C 493	12.8	13.8	33	4	US-08-221-653-104	Sequence 104, App
C 422	13	14.0	48	4	US-09-678-437-39	Sequence 39, Appl	C 494	12.8	13.8	33	4	US-08-442-144A-104	Sequence 104, Appl
C 423	13	14.0	48	5	PCT-US95-00453-8	Sequence 8, Appl	C 495	12.8	13.8	33	4	US-09-472-857-4	Sequence 4, Appl
C 424	13	14.0	49	4	US-09-538-709-1022	Sequence 1022, Ap	C 496	12.8	13.8	33	4	US-09-193-043-87	Sequence 87, Appl
C 425	13	14.0	50	1	US-08-470-123A-3	Sequence 3, Appl	C 497	12.8	13.8	33	4	US-08-991-840A-9	Sequence 9, Appl
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C 430	13	14.0	50	4	US-09-566-591-3	Sequence 3, Appl	C 502	12.8	13.8	33	4	US-09-688-307A-87	Sequence 87, Appl
C 431	13	14.0	50	4	US-09-324-782-6	Sequence 6, Appl	C 503	12.8	13.8	33	4	US-08-661-649-8	Sequence 8, Appl
C 432	13	14.0	50	4	US-09-668-143-6	Sequence 6, Appl	C 504	12.8	13.8	34	1	US-08-283-067-12	Sequence 12, Appl
C 433	13	14.0	50	4	US-09-358-972-252	Sequence 252, Appl	C 505	12.8	13.8	35	1	US-08-283-067-10	Sequence 10, Appl
C 434	12.8	13.8	17	4	US-09-383-316-88	Sequence 88, Appl	C 506	12.8	13.8	35	1	US-08-283-067-52	Sequence 52, Appl
C 435	12.8	13.8	17	4	US-08-117-952-623	Sequence 623, Appl	C 507	12.8	13.8	35	2	US-07-673-661B-9	Sequence 9, Appl
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C 437	12.8	13.8	20	3	US-09-289-267-113	Sequence 113, App	C 509	12.8	13.8	36	1	US-08-309-560-4	Sequence 4, Appl
C 438	12.8	13.8	20	3	US-09-289-267-156	Sequence 156, App	C 510	12.8	13.8	36	2	US-08-975-902-56	Sequence 56, Appl
C 439	12.8	13.8	20	3	US-09-289-267-162	Sequence 162, App	C 511	12.8	13.8	36	2	US-08-491-988-19	Sequence 19, Appl
C 440	12.8	13.8	20	4	US-09-851-062-61	Sequence 61, Appl	C 512	12.8	13.8	36	3	US-08-691-045-47	Sequence 47, Appl
C 441	12.8	13.8	22	1	US-08-487-748A-20	Sequence 20, Appl	C 513	12.8	13.8	36	3	US-09-251-565-56	Sequence 56, Appl
C 442	12.8	13.8	22	2	US-08-480-994-13	Sequence 13, Appl	C 514	12.8	13.8	36	4	US-08-392-459-12	Sequence 12, Appl
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C 449	12.8	13.8	22	3	US-08-398-633-11	Sequence 11, Appl	C 521	12.8	13.8	39	1	US-08-307-619-59	Sequence 59, Appl
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C 451	12.8	13.8	22	3	US-08-829-525-20	Sequence 20, Appl	C 523	12.8	13.8	39	2	US-08-350-260A-105	Sequence 105, App
C 452	12.8	13.8	22	3	US-08-944-496-13	Sequence 13, Appl	C 524	12.8	13.8	39	2	US-08-350-260A-206	Sequence 206, App
C 453	12.8	13.8	22	4	US-08-609-583A-20	Sequence 20, Appl	C 525	12.8	13.8	39	2	US-09-050-783-35	Sequence 59, Appl
C 454	12.8	13.8	22	4	US-08-925-767-13	Sequence 13, Appl	C 526	12.8	13.8	40	2	US-08-628-422-52	Sequence 52, Appl
C 455	12.8	13.8	22	4	US-08-937-399-20	Sequence 20, Appl	C 527	12.8	13.8	40	2	US-08-281-423-16	Sequence 16, Appl
C 456	12.8	13.8	22	4	US-09-560-639-16	Sequence 16, Appl	C 528	12.8	13.8	40	3	US-08-964-020-5	Sequence 5, Appl
C 457	12.8	13.8	22	4	US-09-310-367-20	Sequence 20, Appl	C 529	12.8	13.8	40	4	US-09-225-645-16	Sequence 16, Appl
C 458	12.8	13.8	22	4	US-09-032-337-20	Sequence 20, Appl	C 530	12.8	13.8	41	1	US-08-481-003-6	Sequence 6, Appl
C 459	12.8	13.8	24	1	US-08-468-220-50	Sequence 50, Appl	C 531	12.8	13.8	41	1	US-08-485-598-6	Sequence 15, Appl
C 460	12.8	13.8	24	2	US-08-468-698-50	Sequence 50, Appl	C 532	12.8	13.8	41	3	US-08-906-517-15	Sequence 15, Appl
C 461	12.8	13.8	24	3	US-08-738-168B-6	Sequence 6, Appl	C 533	12.8	13.8	41	4	US-09-262-773-73	Sequence 73, Appl
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C 463	12.8	13.8	24	5	PCT-US94-01533A-50	Sequence 50, Appl	C 535	12.8	13.8	42	4	US-09-290-452-26	Sequence 26, Appl
C 464	12.8	13.8	24	5	PCT-US95-10426-50	Sequence 50, Appl	C 537	12.8	13.8	42	4	US-09-605-785-187	Sequence 787, App
C 465	12.8	13.8	26	2	US-08-859-998-1073	Sequence 1073, Ap	C 538	12.8	13.8	42	4	US-09-290-338-26	Sequence 26, Appl

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540	12.8	13.8	43	2	US-08-050-478-107	Sequence 107, App	613	12.6	13.5	30	4	US-08-687-421-14	Sequence 14, App
541	12.8	13.8	43	4	US-09-414-117-107	Sequence 107, App	614	12.6	13.5	30	4	US-09-179-558-83	Sequence 14, App
542	12.8	13.8	43	4	US-09-678-437-107	Sequence 107, App	615	12.6	13.5	30	4	US-09-377-648-5	Sequence 5, App
543	12.8	13.8	44	1	US-08-530-452-92	Sequence 52, App	616	12.6	13.5	31	1	US-08-375-116A-136	Sequence 136, App
544	12.8	13.8	44	2	US-08-749-852-4	Sequence 4, App	617	12.6	13.5	32	2	US-08-649-511A-10	Sequence 10, App
545	12.8	13.8	44	2	US-08-749-852-4	Sequence 4, App	618	12.6	13.5	32	4	US-09-142-334-7	Sequence 7, App
546	12.8	13.8	44	4	US-08-906-517-52	Sequence 52, App	619	12.6	13.5	32	4	US-09-142-334-7	Sequence 7, App
547	12.8	13.8	45	2	US-08-956-047-88	Sequence 38, App	620	12.6	13.5	32	4	US-09-045-583-44	Sequence 44, App
548	12.8	13.8	45	4	US-09-605-785-786	Sequence 786, App	621	12.6	13.5	32	4	US-08-466-648-44	Sequence 44, App
549	12.8	13.8	46	2	US-08-263-911-19	Sequence 19, App	622	12.6	13.5	32	4	US-09-534-185-55	Sequence 44, App
550	12.8	13.8	46	3	US-09-014-416-13	Sequence 13, App	623	12.6	13.5	32	4	US-09-534-185-55	Sequence 44, App
551	12.8	13.8	47	3	US-08-789-333F-55	Sequence 55, App	624	12.6	13.5	33	6	PCT-US95-04228-44	Patent No. 5338678
552	12.8	13.8	47	4	US-09-338-907-212	Sequence 212, App	625	12.6	13.5	33	6	US-08-975-902-22	Sequence 22, App
553	12.8	13.8	47	4	US-09-218-207-212	Sequence 212, App	626	12.6	13.5	34	3	US-09-251-555-22	Sequence 22, App
554	12.8	13.8	47	4	US-09-641-638-685	Sequence 685, App	627	12.6	13.5	34	3	US-09-243-335-27	Sequence 27, App
555	12.8	13.8	47	4	US-08-787-738B-55	Sequence 55, App	628	12.6	13.5	35	4	US-08-961-083-278	Sequence 278, App
556	12.8	13.8	48	1	US-08-171-389-216	Sequence 216, App	629	12.6	13.5	35	3	US-09-232-278A-17	Sequence 17, App
557	12.8	13.8	48	1	US-08-123-936-216	Sequence 216, App	630	12.6	13.5	35	4	US-07-640-029-7	Sequence 7, App
558	12.8	13.8	48	2	US-08-475-228A-216	Sequence 216, App	631	12.6	13.5	36	1	US-07-640-029-7	Sequence 7, App
559	12.8	13.8	48	3	US-08-482-080A-216	Sequence 216, App	632	12.6	13.5	36	1	US-07-921-807B-18	Sequence 18, App
560	12.8	13.8	48	4	US-09-354-947-216	Sequence 216, App	633	12.6	13.5	36	1	US-07-921-807B-18	Sequence 18, App
561	12.8	13.8	48	5	PCT-US93-12386-216	Sequence 216, App	634	12.6	13.5	36	1	US-08-334-847-736	Sequence 736, App
562	12.8	13.8	49	1	US-08-351-413-15	Sequence 15, App	635	12.6	13.5	36	1	US-08-441-944A-18	Sequence 18, App
563	12.8	13.8	49	2	US-09-025-583-15	Sequence 15, App	636	12.6	13.5	36	3	US-08-856-074A-8	Sequence 8, App
564	12.8	13.8	49	2	US-09-302-620B-59	Sequence 59, App	637	12.6	13.5	36	4	US-08-439-992A-12	Sequence 12, App
565	12.8	13.8	50	2	US-08-989-394-12	Sequence 12, App	638	12.6	13.5	36	4	US-09-302-288-3	Sequence 3, App
566	12.8	13.8	50	4	US-09-271-365-12	Sequence 12, App	639	12.6	13.5	36	4	US-08-218-369-13	Sequence 13, App
567	12.8	13.8	50	4	US-09-604-013A-12	Sequence 12, App	640	12.6	13.5	36	5	PCT-US95-03742-13	Sequence 13, App
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571	12.6	13.5	20	2	US-07-952-277A-31	Sequence 31, App	644	12.6	13.5	38	2	US-08-479-723A-64	Sequence 64, App
572	12.6	13.5	20	2	US-07-952-277A-31	Sequence 31, App	645	12.6	13.5	38	2	US-08-609-230A-6	Sequence 6, App
573	12.6	13.5	20	3	US-08-438-864-4	Sequence 4, App	646	12.6	13.5	38	4	US-09-342-749-19	Sequence 19, App
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575	12.6	13.5	20	4	US-08-628-747-4	Sequence 4, App	648	12.6	13.5	38	5	PCT-US94-04310-64	Sequence 64, App
576	12.6	13.5	20	4	US-09-226-012-44	Sequence 44, App	649	12.6	13.5	39	1	US-07-931-43B-180	Sequence 180, App
577	12.6	13.5	20	4	US-08-402-253-4	Sequence 4, App	650	12.6	13.5	39	1	US-07-714-131C-180	Sequence 180, App
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581	12.6	13.5	20	4	US-09-393-529-9	Sequence 9, App	654	12.6	13.5	39	1	US-08-385-500-11	Sequence 11, App
582	12.6	13.5	20	4	US-09-268-992-28	Sequence 28, App	655	12.6	13.5	39	1	US-08-846-784-11	Sequence 11, App
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584	12.6	13.5	20	4	US-09-705-299-24	Sequence 24, App	657	12.6	13.5	39	2	US-08-469-609A-180	Sequence 180, App
585	12.6	13.5	21	2	US-07-841-591A-7	Sequence 7, App	658	12.6	13.5	39	2	US-08-322-137-93	Sequence 93, App
586	12.6	13.5	21	5	PCT-US93-02034-7	Sequence 134, App	659	12.6	13.5	39	3	US-08-322-137-93	Sequence 93, App
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590	12.6	13.5	22	2	US-08-487-867-29	Sequence 29, App	663	12.6	13.5	40	1	US-08-199-507B-36	Sequence 36, App
591	12.6	13.5	22	2	US-08-187-161-4	Sequence 4, App	664	12.6	13.5	40	1	US-08-441-828-36	Sequence 36, App
592	12.6	13.5	22	3	US-08-464-250-29	Sequence 29, App	665	12.6	13.5	40	2	US-08-875-377-5	Sequence 5, App
593	12.6	13.5	22	3	US-08-757-223-8	Sequence 8, App	666	12.6	13.5	40	4	US-09-312-221A-95	Sequence 95, App
594	12.6	13.5	22	4	US-08-464-250-29	Sequence 29, App	667	12.6	13.5	41	1	US-08-689-190-13	Sequence 13, App
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596	12.6	13.5	24	4	US-09-077-205-4	Sequence 4, App	669	12.6	13.5	41	2	US-08-733-446-50	Sequence 50, App
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598	12.6	13.5	28	2	US-08-840-344-10	Sequence 10, App	671	12.6	13.5	41	2	US-08-835-231-27	Sequence 27, App
599	12.6	13.5	28	3	US-08-622-277A-18	Sequence 18, App	672	12.6	13.5	41	2	US-08-835-231-28	Sequence 28, App
600	12.6	13.5	28	3	US-08-938-830-64	Sequence 64, App	673	12.6	13.5	41	3	US-08-813-507-111	Sequence 111, App
601	12.6	13.5	29	1	US-08-686-878A-55	Sequence 55, App	674	12.6	13.5	41	3	US-08-813-507-122	Sequence 122, App
602	12.6	13.5	29	1	US-08-668-650B-23	Sequence 23, App	675	12.6	13.5	41	4	US-09-108-661-27	Sequence 27, App
603	12.6	13.5	29	4	US-08-686-968C-18	Sequence 18, App	676	12.6	13.5	41	4	US-09-108-661-28	Sequence 28, App
604	12.6	13.5	29	4	US-09-175-928-46	Sequence 46, App	677	12.6	13.5	41	4	US-09-464-453-111	Sequence 111, App
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607	12.6	13.5	30	1	US-08-384-708A-14	Sequence 14, App	680	12.6	13.5	42	1	US-08-709-209-225	Sequence 225, App
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610	12.6	13.5	30	1	US-08-634-826-4	Sequence 4, App	683	12.6	13.5	42	2	US-08-486-969-41	Sequence 41, App
611	12.6	13.5	30	3	US-09-115-175-4	Sequence 4, App	684	12.6	13.5	42	2	US-08-486-969-41	Sequence 41, App

685	12.6	13.5	42	4	US-08-973-124-278	Sequence 278, App	C 758	12.4	13.3	26	4	US-09-610-838-146	Sequence 146, App
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694	12.6	13.5	43	1	US-08-474-633A-94	Sequence 94, App	C 767	12.4	13.3	27	3	US-08-985-162-1055	Sequence 1055, App
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708	12.6	13.5	48	1	US-08-123-936-228	Sequence 228, App	C 781	12.4	13.3	30	2	US-08-583-562B-25	Sequence 25, App
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713	12.6	13.5	48	3	US-08-482-080A-228	Sequence 228, App	C 786	12.4	13.3	30	4	US-09-043-711-13	Sequence 13, App
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752	12.4	13.3	26	1	US-08-472-788A-42	Sequence 42, App	C 825	12.4	13.3	35	1	US-08-090-523-11	Sequence 11, App
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757	12.4	13.3	26	3	US-09-136-389-146	Sequence 146, App	C 830	12.4	13.3	35	2	US-08-475-637-1	Sequence 1, App

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838	12.4	13.3	35	5	PCT-US94-05275-11	Sequence 11, Appl	C 911	12.4	13.3	45	5	PCT-US93-12388-62	Sequence 62, Appl
C 839	12.4	13.3	36	1	US-07-807-529A-46	Sequence 46, Appl	C 912	12.4	13.3	45	5	PCT-US93-12388-62	Sequence 222, Appl
840	12.4	13.3	36	1	US-08-435-350-19	Sequence 19, Appl	C 913	12.4	13.3	45	5	PCT-US94-06197-4	Sequence 4, Appl
841	12.4	13.3	36	1	US-08-300-928C-94	Sequence 94, Appl	C 914	12.4	13.3	45	5	US-08-271-880A-107	Sequence 107, Appl
842	12.4	13.3	36	3	US-08-430-944D-94	Sequence 94, Appl	C 915	12.4	13.3	46	2	US-08-510-408-107	Sequence 107, Appl
C 844	12.4	13.3	36	3	US-08-781-891-108	Sequence 108, Appl	C 916	12.4	13.3	46	2	US-08-249-213-107	Sequence 107, Appl
845	12.4	13.3	36	3	US-08-431-184-94	Sequence 94, Appl	C 917	12.4	13.3	47	2	US-08-495-695B-13	Sequence 13, Appl
C 846	12.4	13.3	36	4	US-09-147-208-38	Sequence 38, Appl	C 918	12.4	13.3	47	3	US-08-155-938-2	Sequence 2, Appl
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C 848	12.4	13.3	37	1	US-08-283-067-35	Sequence 35, Appl	C 920	12.4	13.3	47	4	US-09-338-907-258	Sequence 258, Appl
C 849	12.4	13.3	37	1	US-08-411-796-497	Sequence 497, Appl	C 921	12.4	13.3	47	4	US-09-218-207-258	Sequence 258, Appl
C 850	12.4	13.3	37	3	US-08-471-039-497	Sequence 497, Appl	C 922	12.4	13.3	47	4	US-09-641-638-778	Sequence 778, Appl
C 851	12.4	13.3	37	3	US-09-192-048-3	Sequence 3, Appl	C 923	12.4	13.3	47	4	US-09-641-638-778	Sequence 778, Appl
C 852	12.4	13.3	37	3	US-09-080-044-32	Sequence 32, Appl	C 924	12.4	13.3	47	4	US-09-641-638-778	Sequence 778, Appl
853	12.4	13.3	37	4	US-09-237-712-5	Sequence 3, Appl	C 925	12.4	13.3	47	5	PCT-US94-14436-13	Sequence 13, Appl
C 854	12.4	13.3	37	4	US-09-344-888A-15	Sequence 15, Appl	C 926	12.4	13.3	48	3	US-09-023-082A-45	Sequence 45, Appl
C 855	12.4	13.3	37	4	US-09-531-857A-32	Sequence 32, Appl	C 927	12.4	13.3	48	4	US-09-390-867A-50	Sequence 50, Appl
C 856	12.4	13.3	38	5	PCT-US93-11198-497	Sequence 497, Appl	C 928	12.4	13.3	48	4	US-09-548-260-50	Sequence 50, Appl
C 857	12.4	13.3	38	4	US-09-564-805-167	Sequence 167, Appl	C 929	12.4	13.3	49	3	US-08-388-029A-22	Sequence 22, Appl
C 858	12.4	13.3	39	3	US-08-767-942A-36	Sequence 36, Appl	C 930	12.4	13.3	49	4	US-09-813-781-69	Sequence 69, Appl
C 859	12.4	13.3	40	1	US-08-199-507B-50	Sequence 50, Appl	C 931	12.4	13.3	49	4	US-09-380-190A-37	Sequence 37, Appl
C 860	12.4	13.3	40	1	US-08-441-828-50	Sequence 50, Appl	C 932	12.4	13.3	50	1	US-08-171-389-406	Sequence 406, Appl
C 861	12.4	13.3	40	1	US-08-436-463-12	Sequence 12, Appl	C 933	12.4	13.3	50	1	US-08-231-227-6	Sequence 6, Appl
C 862	12.4	13.3	40	1	US-08-980-032-2	Sequence 2, Appl	C 934	12.4	13.3	50	2	US-08-475-228A-45	Sequence 45, Appl
C 863	12.4	13.3	40	4	US-09-303-064-19	Sequence 19, Appl	C 935	12.4	13.3	50	2	US-08-482-080A-406	Sequence 406, Appl
C 864	12.4	13.3	40	4	US-09-262-773-90	Sequence 90, Appl	C 936	12.4	13.3	50	3	US-08-937-195-17	Sequence 17, Appl
C 865	12.4	13.3	40	4	US-09-086-503-19	Sequence 19, Appl	C 937	12.4	13.3	50	4	US-08-915-152-17	Sequence 17, Appl
C 866	12.4	13.3	40	4	US-09-477-871-2	Sequence 2, Appl	C 938	12.4	13.3	50	4	US-09-194-301-1	Sequence 1, Appl
C 867	12.4	13.3	41	2	US-08-381-637-14	Sequence 14, Appl	C 939	12.4	13.3	50	4	US-08-849-567A-77	Sequence 77, Appl
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C 869	12.4	13.3	42	1	US-08-468-036-24	Sequence 24, Appl	C 941	12.4	13.3	50	4	US-09-261-115-18	Sequence 18, Appl
C 870	12.4	13.3	42	1	US-08-468-036-39	Sequence 39, Appl	C 942	12.4	13.3	50	4	PCT-US93-12388-406	Sequence 406, Appl
C 871	12.4	13.3	42	2	US-08-124-981A-16	Sequence 16, Appl	C 943	12.4	13.3	50	5	PCT-US95-04632-6	Sequence 6, Appl
C 872	12.4	13.3	42	2	US-08-376-843-24	Sequence 24, Appl	C 944	12.4	13.3	50	5	PCT-US96-07627-17	Sequence 17, Appl
C 873	12.4	13.3	42	2	US-08-376-843-39	Sequence 39, Appl	C 945	12.4	13.3	50	5	US-08-717-526-42	Sequence 42, Appl
C 874	12.4	13.3	42	3	US-09-143-270-6	Sequence 6, Appl	C 946	12.2	13.1	17	1	US-09-344-520-12	Sequence 12, Appl
875	12.4	13.3	42	3	US-09-143-270-6	Sequence 7, Appl	C 947	12.2	13.1	18	3	US-09-113-309-5	Sequence 5, Appl
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C 877	12.4	13.3	42	3	US-09-037-190-14	Sequence 14, Appl	C 949	12.2	13.1	18	4	US-09-018-588A-146	Sequence 146, Appl
C 878	12.4	13.3	42	3	US-09-037-192-14	Sequence 14, Appl	C 950	12.2	13.1	18	4	US-09-562-332-5	Sequence 5, Appl
C 879	12.4	13.3	42	3	US-08-295-802-10	Sequence 10, Appl	C 951	12.2	13.1	18	4	US-08-869-423-8	Sequence 8, Appl
C 880	12.4	13.3	42	3	US-09-037-143-14	Sequence 14, Appl	C 952	12.2	13.1	19	1	US-08-502-185-50	Sequence 50, Appl
C 881	12.4	13.3	42	4	US-09-049-691-14	Sequence 14, Appl	C 953	12.2	13.1	19	1	US-08-398-945-50	Sequence 50, Appl
C 882	12.4	13.3	42	4	US-08-260-174-14	Sequence 14, Appl	C 954	12.2	13.1	19	1	US-08-501-779-50	Sequence 50, Appl
C 883	12.4	13.3	42	4	US-08-488-237A-120	Sequence 120, Appl	C 955	12.2	13.1	19	1	US-08-501-779-50	Sequence 50, Appl
C 884	12.4	13.3	42	4	US-09-338-128A-14	Sequence 14, Appl	C 956	12.2	13.1	19	1	US-08-501-779-50	Sequence 50, Appl
C 885	12.4	13.3	42	4	US-08-375-992A-120	Sequence 120, Appl	C 957	12.2	13.1	19	1	US-08-378-860-68	Sequence 68, Appl
C 886	12.4	13.3	42	4	US-09-322-346-14	Sequence 14, Appl	C 958	12.2	13.1	19	1	US-08-501-626-50	Sequence 50, Appl
C 887	12.4	13.3	42	4	US-09-450-083-6	Sequence 6, Appl	C 959	12.2	13.1	19	1	US-08-501-356-50	Sequence 50, Appl
C 888	12.4	13.3	42	4	US-09-450-083-7	Sequence 7, Appl	C 960	12.2	13.1	19	1	US-09-339-913B-68	Sequence 68, Appl
C 889	12.4	13.3	42	4	US-09-037-192-14	Sequence 14, Appl	C 961	12.2	13.1	19	4	US-09-339-913B-68	Sequence 68, Appl
C 890	12.4	13.3	42	4	US-09-155-613A-12	Sequence 12, Appl	C 962	12.2	13.1	19	4	US-09-339-913B-68	Sequence 68, Appl
C 891	12.4	13.3	42	4	US-08-832-985-61	Sequence 61, Appl	C 963	12.2	13.1	19	4	US-09-339-913B-68	Sequence 68, Appl
C 892	12.4	13.3	43	4	US-09-479-123-14	Sequence 14, Appl	C 964	12.2	13.1	19	4	US-08-769-062B-68	Sequence 68, Appl
C 893	12.4	13.3	43	4	US-09-410-903-42	Sequence 42, Appl	C 965	12.2	13.1	19	4	US-08-769-062B-68	Sequence 68, Appl
C 894	12.4	13.3	44	1	US-08-488-702-8	Sequence 8, Appl	C 966	12.2	13.1	19	4	US-09-344-002B-68	Sequence 68, Appl
C 895	12.4	13.3	45	1	US-08-171-389-62	Sequence 62, Appl	C 967	12.2	13.1	19	4	US-09-559-565C-68	Sequence 68, Appl
C 896	12.4	13.3	45	1	US-08-171-389-62	Sequence 62, Appl	C 968	12.2	13.1	19	4	US-09-559-565C-68	Sequence 68, Appl
C 897	12.4	13.3	45	1	US-08-123-936-62	Sequence 22, Appl	C 969	12.2	13.1	20	1	US-08-564-002-2	Sequence 2, Appl
C 898	12.4	13.3	45	1	US-08-123-936-62	Sequence 22, Appl	C 970	12.2	13.1	20	1	US-08-715-142-5	Sequence 5, Appl
C 899	12.4	13.3	45	1	US-08-416-872-4	Sequence 18, Appl	C 971	12.2	13.1	20	3	US-08-281-203-2	Sequence 2, Appl
C 900	12.4	13.3	45	2	US-08-273-146-18	Sequence 62, Appl	C 972	12.2	13.1	20	3	US-08-779-764A-45	Sequence 45, Appl
C 901	12.4	13.3	45	2	US-08-475-228A-62	Sequence 51, Appl	C 973	12.2	13.1	20	4	US-09-180-437-50	Sequence 51, Appl
C 902	12.4	13.3	45	2	US-08-475-228A-62	Sequence 51, Appl	C 974	12.2	13.1	20	4	US-09-180-437-51	Sequence 51, Appl
C 903	12.4	13.3	45	2	US-08-869-793-7	Sequence 7, Appl	C 975	12.2	13.1	20	4	US-09-180-437-51	Sequence 51, Appl
							C 976	12.2	13.1	20	4	US-09-180-437-51	Sequence 51, Appl

c 977 12.2 13.1 20 4 US-09-658-687A-47 Sequence 47, Appl
 978 12.2 13.1 20 4 US-09-387-341-204 Sequence 204, App
 c 979 12.2 13.1 20 4 US-09-844-634-53 Sequence 53, Appl
 980 12.2 13.1 21 1 US-08-050-743-2 Sequence 2, Appl1
 981 12.2 13.1 21 1 US-08-474-542A-7 Sequence 7, Appl1
 982 12.2 13.1 21 1 US-08-457-648-7 Sequence 7, Appl1
 983 12.2 13.1 21 1 US-08-452-055-2 Sequence 2, Appl1
 c 984 12.2 13.1 22 1 US-08-466-033-48 Sequence 48, Appl
 c 985 12.2 13.1 22 1 US-08-444-733-48 Sequence 48, Appl
 c 986 12.2 13.1 22 2 US-08-464-134-48 Sequence 48, Appl
 c 987 12.2 13.1 22 2 US-08-461-361-48 Sequence 48, Appl
 c 988 12.2 13.1 22 2 US-08-485-910-48 Sequence 48, Appl
 989 12.2 13.1 22 4 US-08-430-225A-15 Sequence 15, Appl
 990 12.2 13.1 22 4 US-09-245-041-75 Sequence 75, Appl
 c 991 12.2 13.1 22 5 PCT-US95-06266-32 Sequence 32, Appl
 992 12.2 13.1 23 1 US-08-717-526-18 Sequence 18, Appl
 993 12.2 13.1 24 1 US-08-281-082A-20 Sequence 20, Appl
 c 994 12.2 13.1 24 3 US-08-249-687C-4 Sequence 4, Appl1
 995 12.2 13.1 24 3 US-08-675-887-2 Sequence 2, Appl1
 996 12.2 13.1 25 2 US-08-855-449-9 Sequence 9, Appl1
 c 997 12.2 13.1 25 2 US-09-031-855-3 Sequence 3, Appl1
 c 998 12.2 13.1 25 2 US-08-487-727A-4 Sequence 4, Appl1
 c 999 12.2 13.1 25 4 US-09-385-259-8 Sequence 8, Appl1
 c1000 12.2 13.1 25 4 US-09-645-370-8 Sequence 8, Appl1

ALIGNMENTS

RESULT 1
 US-08-602-716A-8
 ; Sequence 8, Application US/08602716A
 ; Patent No. 5962664
 ; GENERAL INFORMATION:
 ; APPLICANT: FRIEDHOFF, Arnold J.
 ; APPLICANT: BASHAM, Daryl A.
 ; APPLICANT: MILLER, Jeanette C.
 ; TITLE OF INVENTION: PSYCHOSIS PROTECTING NUCLEIC ACID,
 ; TITLE OF INVENTION: PEPTIDES, COMPOSITIONS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,716A
 ; FILING DATE: 23-FEB-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER: US 08/060,560
 ; FILING DATE: 13-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/05545
 ; FILING DATE: 13-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: FRIEDHOFF-1A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 base pairs
 ; TYPE: nucleic acid

; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; US-08-602-716A-8
 ; Query Match 20.0%; Score 18.6; DB 2; Length 45;
 ; Best Local Similarity 84.0%; Pred. No. 1.2e+02;
 ; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 10 GCACCTCATTTGCGCTGGTGACAA 34
 Db 4 GCACCTCATTCACGCTGGTGACAA 28
 RESULT 2
 US-08-331-081B-14
 ; Sequence 14, Application US/08331081B
 ; Patent No. 5998697
 ; GENERAL INFORMATION:
 ; APPLICANT: Devlin, Robert H.
 ; TITLE OF INVENTION: Transgenic Fish and Vectors Therefor
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McFadden, Fincham
 ; STREET: 225 Metcalfe Street, Suite 606
 ; CITY: Ottawa
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: K2P 1P9
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette 3.5 inch, 1.44 MB
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM PC or Compatibles
 ; OPERATING SYSTEM: PC Dos 5.0
 ; SOFTWARE: Wordperfect 5.1 (Patsseq.txt)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/331,081B
 ; FILING DATE: October 20, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: Canada 2,126,138
 ; FILING DATE: June 17, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fincham, H. Ian
 ; REGISTRATION NUMBER: 26,375
 ; REFERENCE/DOCKET NUMBER: 5478-1A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (613) 234-1907
 ; TELEFAX: (613) 234-5233
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-331-081B-14
 ; Query Match 17.8%; Score 16.6; DB 2; Length 30;
 ; Best Local Similarity 82.6%; Pred. No. 6.4e+02;
 ; Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 17 ATTCGCTGCTGGTGACATGCT 39
 Db 7 ATTCAGCTGCTGATGACATGACT 29
 RESULT 3
 US-08-225-224-31/C
 ; Sequence 31, Application US/08225224
 ; Patent No. 5635599
 ; GENERAL INFORMATION:
 ; APPLICANT: PASTAN, Ira
 ; APPLICANT: KREITMAN, Robert J.

;; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
;; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: Steuart Street Tower, One Market Plaza
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: US
;; ZIP: 94105-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/225,224
;; FILING DATE: 8-Apr-1994
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Ellen L.
;; REGISTRATION NUMBER: 32,762
;; REFERENCE/DOCKET NUMBER: 15280-193
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (primer)
;; US-08-225-224-31

Query Match 17.8%; Score 16.6; DB 1; Length 39;
Best Local Similarity 71.0%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGAATGTGACTGTGGGC 73
DB 35 TCTCACACTACCGGAGGTACGAGTGGGCG 5

RESULT 4
US-08-722-258-31/C
;; Sequence 31, Application US/08722258
;; Patent No. 6011002
;; GENERAL INFORMATION:
;; APPLICANT: Pastan, Ira
;; APPLICANT: Kreitman, Robert J.
;; APPLICANT: Puri, Raj K.
;; TITLE OF INVENTION: Circularly Permuted Ligands and
;; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
;; NUMBER OF SEQUENCES: 72
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/722,258
;; FILING DATE: 08-JAN-1997
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US95/04468

;; FILING DATE: 06-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/225,224
;; FILING DATE: 08-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Ellen Lauver
;; REGISTRATION NUMBER: 32,762
;; REFERENCE/DOCKET NUMBER: 015280-193100US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..39
;; OTHER INFORMATION: /note="BK-138 primer"
;; US-08-722-258-31

Query Match 17.8%; Score 16.6; DB 3; Length 39;
Best Local Similarity 71.0%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGAATGTGACTGTGGGC 73
DB 35 TCTCACACTACCGGAGGTACGAGTGGGCG 5

RESULT 5
PCT-US95-04468-31/C
;; Sequence 31, Application PC/TUS9504468
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
;; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
;; NUMBER OF SEQUENCES: 59
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04468
;; FILING DATE: 07-APR-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/225,224
;; FILING DATE: 08-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Ellen L.
;; REGISTRATION NUMBER: 32,762
;; REFERENCE/DOCKET NUMBER: 15280-193-1PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 39 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (primer)
;; PCT-US95-04468-31

Query Match 17.8%; Score 16.6; DB 5; Length 39;
Best Local Similarity 71.0%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;


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1 COMPUTER: IBM compatible
2 OPERATING SYSTEM: MS-DOS
3 SOFTWARE: WordPerfect 6.0
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/08/687,421
6 FILING DATE: 08-MAY-1996
7 CLASSIFICATION: 435
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER:
10 FILING DATE: 08/195,005
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER:
13 FILING DATE: 10-FEBRUARY-1994
14 APPLICATION NUMBER:
15 FILING DATE: 22-APRIL-1993
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/219,012
18 FILING DATE: 28-MARCH-1994
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 07/973,333
21 FILING DATE: 11-NOVEMBER-1992
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 07/714,131
24 FILING DATE: 10-JUNE-1991
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/536,428
27 FILING DATE: 11-JUNE-1990
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Barry J. Swanson
30 REGISTRATION NUMBER: 33,215
31 REFERENCE/DOCKET NUMBER: NEX07/PCT
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (303) 793-3333
34 TELEFAX: (303) 793-3433
35 INFORMATION FOR SEQ ID NO: 5:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 50 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
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Query Match	17.88;	Score 16.6;	DB 4;	Length 50;
Best local similarity	71.08;	Pred. No. 8.2e-02;		
Matches	22;	Conservative	0;	Mismatches 9;
				Indels 0;
				Gaps 0;
Qy	49	CACATCGAATGTGACTGTGGGGCTTCAG	79	
Db	20	CACATATGGGAGATGCTCTTCGACGATGTCG	50	

RESULT 9
 US-08-957-001B-19/c
 : Sequence 19, Application US/08957001B
 : Patent No 6228621
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Williams, William V.
 : APPLICANT: Madalo, Michael
 : APPLICANT: Welner, David B.
 : TITLE OF INVENTION: IMPROVED VACCINES
 : NO. OF SEQUENCES: 27
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621rist
 :
 : STREET: One Liberty Place, 46th floor
 : City: Philadelphia
 : STATE: Pennsylvania
 : COUNTRY: USA
 :
 : ZIP: 19103
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Windows
 : SOFTWARE: wordperfect
 :
 : CURRENT APPLICATION DATA:
 :
 : APPLICATION NUMBER: US/08/957,001B
 :

FILING DATE: 23-OCT-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/029,592
 FILING DATE: 23-OCT-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: UPV-3303
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 47 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 OS-08-957-001B-19

	Query Match	17.68;	Score 16.4;	DB 4;	Length 47;
	Best Local Similarity	60.58;	Pred. No. 9,	6e-02;	
Matches	23; Conservative	2;	Mismatches	13;	Indels 0; Gaps 0;
OY	55 CGGATGTGACTGTCGGGCCCTCGAGAAAACATTGAGCT	92			
	: : :	: : :			
Dd	46 CAGRTGYTGACGCTGGACCCTCGATTGAACATTTTAAAT	9			

RESULT 10
 US-09-496-301-19/c
 : Sequence 19, Application US/09496301
 : Patent No. 6248565
 :
 GENERAL INFORMATION:
 APPLICANT: Williams, William V.
 APPLICANT: Madalo, Michael
 APPLICANT: Weiner, David B.
 TITLE OF INVENTION: IMPROVED VACCINES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565Stris
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 :
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: windows
 SOFTWARE: wordperfect
 :
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/496,301
 FILING DATE:
 :
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/957,001
 FILING DATE: 23-OCT-1997
 APPLICATION NUMBER: US 60/029,592
 FILING DATE: 23-OCT-1996
 :
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: UPN-3303
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 :
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 47 base pairs
 :

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-496-301-19

Query Match 17.6%; Score 16.4; DB 4; Length 47;
Best Local Similarity 60.5%; Pred. No. 9.6e+02;
Matches 23; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 55 CGGAGTGTACTGTGGCCCTCCAGAAACATGTAGGT 92
DB 46 CAGTGTGTGACGTGACCTCTGATTAAGATTGAT 9

RESULT 11
US-08-778-494B-103/C
Sequence 103, Application US/0878494B
Patent No. 5962272

GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Zhu, Jork
APPLICANT: Diachenko, Luda
APPLICANT: Siebert, Paul
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR FULL-LENGTH CDNA
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESS: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,494B
FILING DATE: 03-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/582,562
FILING DATE: 03-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doan R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CL-7C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-778-494B-103

Query Match 17.4%; Score 16.2; DB 2; Length 40;
Best Local Similarity 64.9%; Pred. No. 1.1e+03;
Matches 24; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 3 GCTGGAGCAGCTCATTCCTGCTGGGTGACATGCTT 39
DB 37 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTACCACTCTT 1

RESULT 12
US-09-276-533A-10/C

Sequence 10, Application US/09276533A
Patent No. 6436707
GENERAL INFORMATION:
APPLICANT: Zambrowicz, Brian
APPLICANT: Friedrich, Glenn A.
APPLICANT: Lalleberg, Stan
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: VECTORS FOR GENE MUTAGENESIS AND GENE
FILE REFERENCE: 07/05-0006-00000
CURRENT APPLICATION NUMBER: US/09/276,533A
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 60/079,729
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/081,727
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/109,302
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 39
TYPE: DNA
ORGANISM: Mus musculus
US-09-276-533A-10

Query Match 17.0%; Score 15.8; DB 4; Length 39;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 67 GTCGGCTCCAGAAACATTGAGTG 93
DB 33 GCGGCTCTGCGACGAGGACAGTGGGTG 7

RESULT 13
US-09-237-712-6/C
Sequence 6, Application US/09237712
Patent No. 6180391
GENERAL INFORMATION:
APPLICANT: BROWN, WILLIAM C.
TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS
FILE REFERENCE: A-518
CURRENT APPLICATION NUMBER: US/09/237,712
CURRENT FILING DATE: 1999-01-26
EARLIER APPLICATION NUMBER: 60/072,794
EARLIER FILING DATE: 1998-01-28
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 40
TYPE: DNA
ORGANISM: oligonucleotide
US-09-237-712-6

Query Match 17.0%; Score 15.8; DB 4; Length 40;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 CACTCATTCCTGCTGGGTGACATGCTT 37
DB 27 CACTCATTCCTGCTGGGTGACATGCTT 1

RESULT 14
US-08-613-507-45/C
Sequence 45, Application US/08613507
Patent No. 6114116
GENERAL INFORMATION:
APPLICANT: Lemieux, Bertrand
APPLICANT: Landry, Benoit S.
APPLICANT: Sapolsky, Ronald J.

TITLE OF INVENTION: Brassica Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,507
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,069
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-030100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: variation
LOCATION: replace(21, "")
OTHER INFORMATION: /note="deletion polymorphism"
US-08-813-507-45

Query Match 17.0%; Score 15.8; DB 3; Length 42;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGAATGACTGTC 69
DB 32 TTGGACTCTGTGGACTGTACTGTC 6

RESULT 15
US-09-464-453-45/c
Sequence 45, Application US/09464453
Patent No. 6358686
GENERAL INFORMATION:
APPLICANT: Lemieux, Bertrand
Landry, Benoit S.
Sapolsky, Ronald J.
TITLE OF INVENTION: Brassica Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/464,453
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/813,507
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-030100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: variation
LOCATION: replace(21, "")
OTHER INFORMATION: /note="deletion polymorphism"
US-09-464-453-45

Query Match 17.0%; Score 15.8; DB 4; Length 42;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGAATGACTGTC 69
DB 32 TTGGACTCTGTGGACTGTACTGTC 6

RESULT 16
US-08-368-395-8/c
Sequence 8, Application US/08368395
Patent No. 5631150
GENERAL INFORMATION:
APPLICANT: Haikl, Anu M.
APPLICANT: Myasnikov, Andrey N.
APPLICANT: Apajalhti, Juh A.
APPLICANT: Pastinen, Ossi A.
TITLE OF INVENTION: Manufacture of xyliol
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,395
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,672
FILING DATE: 24-AUG-1993
APPLICATION NUMBER: US 07/973,325
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1427.0010001
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-368-395-8

Query Match 17.0%; Score 15.8; DB 1; Length 44;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 8 GAGACTCCATTCGCTGCTGACAA 34
DB 39 GACCATTCATCTATAAGGTGACAA 13

RESULT 17

US-08-285-936-14
Sequence 14, Application US/08285936
Patent No. 5728821
GENERAL INFORMATION:
APPLICANT: Yelton, Dale
APPLICANT: Glaser, Scott
APPLICANT: Huse, William
APPLICANT: Rosok, Mae J.
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,936
FILING DATE: 04-AUG-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Adilano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.160S01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-285-936-14

Query Match 16.8%; Score 15.6; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 70 GGGCTCCAGAAACATGTAGG 91
DB 2 GGGACTCCAGAAACCTTTAGG 23

RESULT 18

US-08-487-860-14
Sequence 14, Application US/08487860
Patent No. 5792456
GENERAL INFORMATION:
APPLICANT: Yelton, Dale
APPLICANT: Glaser, Scott
APPLICANT: Huse, William
APPLICANT: Rosok, Mae J.
TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,860
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Adilano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.160S01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-9031
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-487-860-14

Query Match 16.8%; Score 15.6; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 70 GGGCTCCAGAAACATGTAGG 91
DB 2 GGGACTCCAGAAACCTTTAGG 23

RESULT 19

US-09-103-875-10
Sequence 10, Application US/09103875A
Patent No. 6221849
GENERAL INFORMATION:
APPLICANT: Szyf, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES
FILE REFERENCE: 106101.194
CURRENT APPLICATION NUMBER: US/09/103,875A
CURRENT FILING DATE: 1998-06-24
EARLIER APPLICATION NUMBER: 60/069,865
EARLIER FILING DATE: 1997-12-17
EARLIER APPLICATION NUMBER: 08/866,340
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 43

TYPE: DNA
ORGANISM: Homo sapiens
US-09-103-875-10

Query Match
Best Local Similarity 70.0%; Pred. No. 26+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

18 TTCTGCTGGTGGACATGCTTGTTC 47
||||| ||||| ||| ||||| |||
8 TTCTGCTGGTGGTGTGTTCTTGTTC 37

RESULT 20
US-08-973-124-285
Sequence 285, Application US/08973124
Patent No. 6207816

GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
NUMBER OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluor

US-08-973-124-285

Query Match
Best Local Similarity 52.0%; Pred. No. 2,36+03;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

30 GACATGCGCTTGTTCACACAT 54
||||| :||| :||| :||| :|||
4 GACATGCGCGGCGGUCGCAUUCU 28

RESULT 21
PCT-US96-08014-285
Sequence 285, Application PC/TUS9608014

GENERAL INFORMATION:
APPLICANT: LARRY GOLD; NEBOJSA JANJIC; STEVEN RINGQUIST; NIKOS
APPLICANT: PAGRATIS, PENELOPE J. TOOTHMAN
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR (KGF)
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 285;
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F) modified
PCT-0896-08014-285

Query Match
Best Local Similarity 52.08; Score 15.4; DB 5; Length 41;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 30 GACATGCTGCTGCTGACACTAT 54
DB 4 GACGAGCGGUGUCUACAUUCU 28

RESULT 22

US-08-454-557C-63/C
Sequence 63, Application US/08454557C
Patent No. 5830670

GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both

US-08-454-557C-63

Query Match
Best Local Similarity 85.08; Score 15.2; DB 2; Length 31;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTCAGCTGGGTGACAGAC 8

RESULT 23
US-08-340-426D-63/C
Sequence 63, Application US/08340426D

PATENT NO. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both

US-08-340-426D-63

Query Match
Best Local Similarity 85.08; Score 15.2; DB 2; Length 31;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTCAGCTGGGTGACAGAC 8

RESULT 24

US-08-450-673C-63/C
Sequence 63, Application US/08450673C
Patent No. 5948888

GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-450-673C-63

Query Match 16.3%; Score 15.2; DB 2; Length 31;
Best Local Similarity 85.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTGAGCTGGGTGACAGAC 8

RESULT 25
PCT-US95-17111A-63/c
Sequence 63, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
PCT-US95-17111A-63

Query Match 16.3%; Score 15.2; DB 5; Length 31;
Best Local Similarity 85.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 18 TTCTGCTGGGTGACATGC 37
DB 27 TTGAGCTGGGTGACAGAC 8

DB 27 TTCAGCTGGGTGACAGAC 8
RESULT 26
US-09-344-700-21
Sequence 21, Application US/09344700
Patent No. 6265194
GENERAL INFORMATION:
APPLICANT: Nezu, Jun-ichi
APPLICANT: Oku, Asuka
TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE
FILE REFERENCE: 06501/035001
CURRENT APPLICATION NUMBER: US/09/344,700
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: PCT/JP97/0485
EARLIER FILING DATE: 1997-12-25
EARLIER APPLICATION NUMBER: JP 8/357864
EARLIER FILING DATE: 1996-12-27
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 36
TYPE: DNA
ORGANISM: Homo sapiens
US-09-344-700-21

Query Match 16.3%; Score 15.2; DB 4; Length 36;
Best Local Similarity 63.9%; Pred. No. 2.7e+03;
Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 ACCTGGAGCACATCTGCTGGGTGACATGC 37
DB 1 ACCTGGAGCACATCTGCTGGGTGACATGC 36

RESULT 27
PCT-US94-14888-4/c
Sequence 4, Application PC/TUS9414888
GENERAL INFORMATION:
APPLICANT: Cell Genesys, Inc.
TITLE OF INVENTION: Homologous Recombination for Universal
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14888
FILING DATE: 28 DEC 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: FP-55190-4/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA


```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,802
FILING DATE: Herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bovine respiratory syncytial virus
STRAIN: Strain 375
US-08-295-802-143

Query Match
Best Local Similarity 16.1%; Score 15; DB 3; Length 41;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 33 AATGCTTGTTTCACACTATCGGATGTG 63
DB 40 AATGCTTGATTTAAGATGATGCGTATGAG 10

RESULT 36
US-08-686-968C-70/c
Sequence 70, Application US/08686968C
Patent No. 6221361
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 70
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-686-968C-70

Query Match
Best Local Similarity 16.1%; Score 15; DB 4; Length 41;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 33 AATGCTTGTTTCACACTATCGGATGTG 63
DB 40 AATGCTTGATTTAAGATGATGCGTATGAG 10

RESULT 37
US-08-488-237A-143/c
Sequence 143, Application US/08488237A
Patent No. 6251403
GENERAL INFORMATION:
```

```
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,237A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bovine respiratory syncytial virus
STRAIN: Strain 375
US-08-488-237A-143

Query Match
Best Local Similarity 16.1%; Score 15; DB 4; Length 41;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 33 AATGCTTGTTTCACACTATCGGATGTG 63
DB 40 AATGCTTGATTTAAGATGATGCGTATGAG 10

RESULT 38
US-08-672-213-30
Sequence 30, Application US/08672213
Patent No. 630649
GENERAL INFORMATION:
APPLICANT: Gilman, Michael Z.
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139-4234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
```

```

1      FILING DATE: 27-JUN-1996
2      CLASSIFICATION: 514
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 60/000,553
5      FILING DATE: 27-JUN-1995
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER: US 60/019,614
8      FILING DATE: 29-DEC-1995
9      ATTORNEY/AGENT INFORMATION:
10     NAME: BERSTEIN, David L.
11     REGISTRATION NUMBER: 31,235
12     REFERENCE/DOCKET NUMBER: ARIAD 346B
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: 617-494-0400
15     TELEFAX: 617-494-0208
16     INFORMATION FOR SEQ ID NO: 30:
17     SEQUENCE CHARACTERISTICS:
18     LENGTH: 41 base pairs
19     TYPE: nucleic acid
20     STRANDEDNESS: single
21     TOPOLOGY: linear
22     MOLECULE TYPE: cDNA
23     FEATURE:
24     NAME/KEY: CDS
25     LOCATION: 1..40
26     OS-08-672-213-30

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Query Match      16.1%; Score 15; DB 4; Length 41;
Best Local Similarity 67.7%; Pzed. No. 3.4e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

      45 TCACACTATCGCAATGTACTGTCGGCCT 75
      |||||
      5 TCACACTAGAGAGATGTGCTGAAGCCT 35

```

RESULT 39
 US-08-1375-992A-143/C
 Sequence 143 Application US/08375992A
 Patent No. 6328975
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 APPLICANT: Junker, David E.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 220
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/375,992A
 FILING DATE: Herewith
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 143:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 41 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

? MOLECULE TYPE: DNA (genomic)
 ? HYPOTHEetical: NO
 ? ANTI-SENSE: NO
 ? ORIGINAL SOURCE:
 ? ORGANISM: Bovine respiratory syncytial virus
 ? STRAIN: Strain 3/5
 ? OS-08-375-992A-143

Query Match	16.1%	Score 15;	DB 4;	Length 41;
Best Local Similarity	67.7%;	Pred. No. 3.4e+03;		
Matches 21; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

```

QY      33 AATGCCCTTGGTTTCAACACTATCGGATGTG 63
        ||| ||| | | | | | | | |
Db      40 AATGCTTGAAATTAAAGATGATGGGTAG 100

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RESULT 40
US-08-596-387B-38
; Sequence 38, Application US/08596387B

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent In Release #1.0, Vers1
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/596,387B
8 FILING DATE:
9 CLASSIFICATION: 435
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: PCT/US95/09816
12 FILING DATE: 31-JUL-1995
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/382,454
15 FILING DATE: 01-FEB-1995
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/283,302
18 FILING DATE: 29-JUL-1994
19 APPLICATION NUMBER: US 08/283,302
20 FILING DATE: 29-JUL-1994
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Pearson, Louise S.
23 REGISTRATION NUMBER: 32,369
24 REFERENCE/DOCKET NUMBER: STR-4605-CIP22
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (708) 267-5300
27 TELEFAX: (708) 267-5376
28 INFORMATION FOR SEQ. ID NO.: 38:
29 SOURCE CHARACTERISTICS:
30 LENGTH: 42 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: unknown
33 TOPOLOGY: unknown
34
35 US-08-596-387B-38

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Query Match	10.1%	Score 15;	DB 2;	Length 42;
Best Local Similarity	67.7%	Pred. No. 3.4e+03;		
Matches 21;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
0y	11	CACTCCATTTCGCTGGGTGACATGCTTG	41	

Db 1 ||||| ||||| ||||| ||||| |||||
1 CCCCCAGGCTTCCGGGCGCACCATGCGGTG 31

RESULT 41

US-09-067-615-38

Sequence 38, Application US/09067615

Patent No. 6309645

GENERAL INFORMATION:

APPLICANT: Rhode, Peter R.

APPLICANT: Jiao, Jin-An

APPLICANT: Burkhardt, Martin

APPLICANT: Wong, Hing

TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dade International, Inc.

STREET: 1717 Deerfield Road

CITY: Deerfield

STATE: Illinois

COUNTRY: USA

ZIP: 60015

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/067,615

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/596,387

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/382,454

FILING DATE: 01-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,302

FILING DATE: 29-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Pearson, Louise S.

REGISTRATION NUMBER: 32,369

REFERENCE/DOCKET NUMBER: STR-4665-CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 267-5300

TELEFAX: (708) 267-5376

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

US-09-067-615-38

US-09-067-615-38

US-09-067-615-38

US-09-067-615-38

US-09-067-615-38

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US-09-067-615-38

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US-09-067-615-38

APPLICANT: Chavallaz, Pierre-Andre
APPLICANT: Jiao, Jin-An
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dade International, Inc.

STREET: 1717 Deerfield Road

CITY: Deerfield

STATE: Illinois

COUNTRY: USA

ZIP: 60015

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09816A

FILING DATE: 31-JUL-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/382,454

FILING DATE: 01-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,302

FILING DATE: 29-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Pearson, Louise S.

REGISTRATION NUMBER: 32,369

REFERENCE/DOCKET NUMBER: STR-4665-CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 267-5300

TELEFAX: (708) 267-5376

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

PCT-US95-09816A-38

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PCT-US95-09816A-38

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PCT-US95-09816A-38

PCT-US95-09816A-38

APPLICANT: Chavallaz, Pierre-Andre
APPLICANT: Jiao, Jin-An
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dade International, Inc.

STREET: 119 NORTH FOURTH STREET, SUITE 201

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/681,935

FILING DATE: 31-JUL-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/382,454

FILING DATE: 01-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,302

FILING DATE: 29-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Pearson, Louise S.

REGISTRATION NUMBER: 32,369

REFERENCE/DOCKET NUMBER: STR-4665-CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 267-5300

TELEFAX: (708) 267-5376

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

PCT-US95-09816A-38

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PCT-US95-09816A-38

FILING DATE: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, MYRA H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 140,00040101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1225
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-681-935-13

Query Match 16.1%; Score 15; DB 1; Length 45;
Best Local Similarity 61.5%; Pred. No. 3.6e+03;
Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 30 GACATGCTTGGTTGACACATACGAAATGACTG 68
Db 7 GTCCACGATTCCTTTGACAGATGCGATTTGATAGT 45

RESULT 44
US-08-939-323-13
Sequence 13, Application US/08939323
Patent No. 6255462
GENERAL INFORMATION:
APPLICANT: GROSE, CHARLES F.
TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND
TITLE OF INVENTION: IMMUNOPURIFICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTTING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,323
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/681,935
FILING DATE: 29-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOTTING MS., ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 140,00040102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1217
TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-939-323-13

Query Match 16.1%; Score 15; DB 4; Length 45;
Best Local Similarity 61.5%; Pred. No. 3.6e+03;

Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 30 GACATGCTTGGTTGACACATACGAAATGACTG 68
Db 7 GTCCACGATTCCTTTGACAGATGCGATTTGATAGT 45

RESULT 45
US-08-584-040-3659/c
Sequence 3659, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3659:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "N" represents the stem II region
OTHER INFORMATION: of an HH ribozyme.
US-08-584-040-3659

Query Match 15.9%; Score 14.8; DB 4; Length 27;
Best Local Similarity 70.4%; Pred. No. 3.4e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 61 GTGACTGTGCGGCTTCAGAAACATT 87
Db 27 GTGAGTGTTCNCTCAGCAAAACATT 1

RESULT 46
US-08-584-040-5068/c

```
; Sequence 5068, Application US/08584040
; Patent No 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Walburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5068:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The letter "N" represents the stem II region
; OTHER INFORMATION: of an HH ribozyme.
US-08-584-040-5068

OY 61 GTGACTGTGGGGCCGAGAAACATT 87
Db 27 GTGAGTCTTCATCATCAGAAACATT 1

Query Match 15.9%; Score 14.8; DB 4; Length 27;
Best Local Similarity 70.4%; Pred. No. 3.4e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,457
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-562A-33

OY 44 TTTCACACATTCGAGATGTCATGTC 69
Db 3 TTTCAGCTATTGACAGCTGATGTC 28

Query Match 15.9%; Score 14.8; DB 2; Length 30;
Best Local Similarity 73.1%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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RESULT 47
US-08-332-562A-33
; Sequence 33, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.
; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.

RESULT 48
US-08-813-507-147
; Sequence 147, Application US/08813507
; Patent No. 6114116
; GENERAL INFORMATION:
; APPLICANT: Lemieux, Bertrand
; APPLICANT: Landry, Benoit S.
; APPLICANT: Sapolsky, Ronald J.
; TITLE OF INVENTION: Brassaica Polymorphisms
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,507
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
```

APPLICATION NUMBER: US 60/032,069
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-03010005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200

TELEX:
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-813-507-147
Query Match 15.9%; Score 14.8; DB 3; Length 41;
Best Local Similarity 61.1%; Pred. No. 4.1e+03;
Matches 22; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 28 GTGACATGCTTGGTTTCACACTATCGAATGTG 63
DB 6 GTGAAAGCATTTGTCCTCCAAATCTCGCTGTGCG 41

RESULT 49

US-09-464-453-147
Sequence 147, Application US/09464453
Patent No. 6358686

GENERAL INFORMATION:
APPLICANT: Lemieux, Bertrand

Landry, Benoit S.
Sapolsky, Ronald J.
TITLE OF INVENTION: Brassicac Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/464,453

FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/813,507

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-03010005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200

TELEFAX: 415 576-0200

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 147:
US-09-464-453-147

Query Match 15.9%; Score 14.8; DB 4; Length 41;
Best Local Similarity 61.1%; Pred. No. 4.1e+03;
Matches 22; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 28 GTGACATGCTTGGTTTCACACTATCGAATGTG 63
DB 6 GTGAAAGCATTTGTCCTCCAAATCTCGCTGTGCG 41

RESULT 50

US-07-963-331D-5
Sequence 5, Application US/07963331D
Patent No. 5334511

GENERAL INFORMATION:
APPLICANT: Harada, Yasuhiro

APPLICANT: Nakano, Eiichi
APPLICANT: Tatsumi, Hiroki

APPLICANT: Imezumi, Motoaki

TITLE OF INVENTION: Isolated Mink Growth

TITLE OF INVENTION: Hormone Genes, No. 5334511e1 Recombinant DNA And

TITLE OF INVENTION: Methods for Producing Mink Growth Hormone.

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building

CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,

SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/963,331D
FILING DATE: 19921016

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Dergosits, Michael E.
REGISTRATION NUMBER: 31,243

REFERENCE/DOCKET NUMBER: HIRA-00600
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716

TELEX: 278356

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 45
TYPE: NUCLEIC ACID

STRANDEDNESS: Single-stranded
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid (synthesized
MOLECULE TYPE: DNA)

FEATURE:
OTHER INFORMATION: Based on the base sequence

OTHER INFORMATION: of rat growth
OTHER INFORMATION: hormone

US-07-963-331D-5

Query Match 15.9%; Score 14.8; DB 1; Length 45;
Best Local Similarity 73.1%; Pred. No. 4.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 TTCTGCTGCTGGTGACATGCTTGTGT 43
DB 19 TCCAGCTGTTGCGAATGCGCTGTCT 44

RESULT 51

US-09-167-681-6
Sequence 6, Application US/09167681A

Patent No. 6265561
GENERAL INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raflogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: O'Brien, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-167-681-6

Query Match 15.7%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 15 CCATCTGCTGCTGGTGCACAT 35
DB 1 CCACCTGCTGCTGGCCACACAT 21

RESULT 52
US-09-167-681-12
Sequence 12, Application US/09167681A
Patent No. 6265561
GENERAL INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raflogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: O'Brien, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-167-681-12

Query Match 15.7%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 15 CCATCTGCTGCTGGTGCACAT 35
DB 1 CCACCTGCTGCTGGCCACACAT 21

RESULT 53
US-08-557-128-23
Sequence 23, Application US/08557128
Patent No. 5849524
GENERAL INFORMATION:
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: MISAWA, No. 5849524ihiko
TITLE OF INVENTION: TRANSFORMATION SYSTEMS FOR THE YEAST
TITLE OF INVENTION: CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
TITLE OF INVENTION: THEREWITH
NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,128
FILING DATE: 25-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/01005
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-129287
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-285823
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-135015
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/108
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-557-128-23

Query Match 15.7%; Score 14.6; DB 2; Length 31;
Best Local Similarity 81.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CTGGGAGCAGCTCCATCTGCC 24
DB 10 CAGCGAGCAGCTCAATCTGCC 30

RESULT 54
US-08-564-109C-15/c
Sequence 15, Application US/08564109C
Patent No. 6018103
GENERAL INFORMATION:
APPLICANT: Filipowicz, Witold
APPLICANT: Connelly, Sheila
TITLE OF INVENTION: Chimeric Plant Genes Possessing
TITLE OF INVENTION: Independent Regulatory Sequences
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018103artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,109C
FILING DATE: 15-DEC-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hehman, Mary K.
REGISTRATION NUMBER: 39,206
REFERENCE/DOCKET NUMBER: S-19593/A/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8525
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-564-109C-15

Query Match 15.7%; Score 14.6; DB 3; Length 33;
Best Local Similarity 69.0%; Pred. No. 4.5e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 20 CTGCTGGGTGACATGCTTGTTTCAA 48
DB 31 CGGCCGCGCCCAATGATGGGCCAA 3

RESULT 55
5504194-4/C
PATENT NO. 5504194
APPLICANT: ST. JOHN, THOMAS P.; GALLATIN, W. MICHAEL; IDZERA, NEDEAN
TITLE OF INVENTION: LYMPHOCYTE ADHESION RECEPTOR FOR HIGH
ENDOTHELIUM, CD4
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,624
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 628,646
FILING DATE: 12-DEC-1990
APPLICATION NUMBER: 325,224
FILING DATE: 17-MAR-1989
SEQ ID NO: 4
LENGTH: 33
5504194-4

Query Match 15.7%; Score 14.6; DB 6; Length 33;
Best Local Similarity 69.0%; Pred. No. 4.5e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 20 CTGCTGGGTGACATGCTTGTTTCAA 48
DB 31 CGGCCGCGCCCAATGATGGGCCAA 3

RESULT 56
US-08-683-877-7/C
Sequence 7, Application US/08683877
Patent No. 5776689
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Elledge, Stephen J.
APPLICANT: Aronheim, Ami
TITLE OF INVENTION: Protein Recruitment System
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,877
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1971
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-683-877-7

Query Match 15.7%; Score 14.6; DB 1; Length 35;
Best Local Similarity 69.0%; Pred. No. 4.6e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 7 GGAGACATCATCTGCTGGTGACAT 35
DB 33 CGAGCACC CGGCTCCCGGTGACAT 5

RESULT 57
US-08-683-877-9/C
Sequence 9, Application US/08683877
Patent No. 5776689
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Elledge, Stephen J.
APPLICANT: Aronheim, Ami
TITLE OF INVENTION: Protein Recruitment System
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,877
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1971
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-683-877-9

Query Match 15.7%; Score 14.6; DB 1; Length 35;
Best Local Similarity 69.0%; Pred. No. 4.6e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 7 GGAGCACTCATCTGCTGGTGACAAAT 35
DB 33 GGAGCACTCATCTGCTGGTGACAAAT 5

RESULT 58
US-09-242-690A-30
; Sequence 30, Application US/09242690A
; Patent No. 6284534
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/242,690A
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02924
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: JP 8/241062
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-242-690A-30

Query Match 15.7%; Score 14.6; DB 4; Length 38;
Best Local Similarity 81.0%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 CTGGAGCACTCATCTGCTGCC 24
DB 17 CAGCGAGCACTCAAACTGCTGC 37

RESULT 59
US-08-431-080-9
; Sequence 9, Application US/08431080
; Patent No. 5698686
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/431,080
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: SN 08/326,781
;; FILING DATE: October 20, 1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parker, David L.
;; REGISTRATION NUMBER: 32,165
;; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (713) 789-2679
;; TELEX: 79-0924
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-431-080-9

Query Match 15.7%; Score 14.6; DB 1; Length 40;
Best Local Similarity 69.0%; Pred. No. 4.9e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 63 GACTGCTGGGCTCCGAAACATGAGG 91
DB 6 GACTGCTGGCTCGTCAAAAATTTCAGG 34

RESULT 60
US-08-185-949B-99/C
; Sequence 99, Application US/08185949B
; Patent No. 5874279
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; APPLICANT: Richard D. Macdonald
; TITLE OF INVENTION: Recombinant Infectious Bovine
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,949B
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 278-0525
; INFORMATION FOR SEQ ID NO: 99:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-185-949B-99

Query Match 15.7%; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.0%; Pred. No. 4.9e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 33 ATGCGTGTTCACACTATCGGATG 61
DB 39 ATGCTGTGAATTTAGATGATGCTATG 11

RESULT 61
US-08-938-534-9

Sequence 9, Application US/08938534
Patent No. 5916752

GENERAL INFORMATION:

APPLICANT: Gottschling, Daniel E.

APPLICANT: Singer, Miriam S.

TITLE OF INVENTION: Telomerase Compositions and Methods

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TEXAS

COUNTRY: UNITED STATES OF AMERICA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,534

FILING DATE: 26-SEP-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/431,080

FILING DATE:

APPLICATION NUMBER: SN 08/326,781

FILING DATE: October 20, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: ARCD:155/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-938-534-9

Query Match 15.7%; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.0%; Pred. No. 4.9e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 63 GACTGTGCGGCTCCAGAAACATGAGG 91
DB 6 GACTGTGCTCCGTCAGAAAAAATTTCAAGG 34

RESULT 62
US-08-778-494B-100/c
Sequence 100, Application US/08778494B
Patent No. 5962272
GENERAL INFORMATION:

APPLICANT: Chenchik, Alex
APPLICANT: Zhu, York
APPLICANT: Diachenko, Luda
APPLICANT: Siebert, Paul
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR FULL-LENGTH CDNA
NUMBER OF SEQUENCES: 114
CLONING

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st street, suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/778,494B

FILING DATE: 03-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/582,562

FILING DATE: 03-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Doran R.

REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: CL-701

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

US-08-778-494B-100

Query Match 15.7%; Score 14.6; DB 2; Length 40;
Best Local Similarity 62.2%; Pred. No. 4.9e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 3 GCTGGAGCACCTCCATTCGCTGGTGACATGCT 39
DB 37 GCTGCTGCTGCCCACTCTGCTGTGACCATGCTT 1

RESULT 63
US-08-483-511-80
Sequence 80, Application US/08483511
Patent No. 6297048

GENERAL INFORMATION:

APPLICANT: Jolly, Douglas J.

APPLICANT: Chang, Stephen M.W.

APPLICANT: Lee, William T.L.

APPLICANT: Townsend, Kay

APPLICANT: O'Dea, Joanne

TITLE OF INVENTION: HEPATITIS THERAPEUTICS

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: U.S.

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,511
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049,407C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-511-80

Query Match 15.7%; Score 14.6; DB 4; Length 40;
Best Local Similarity 81.0%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 72 GCCTCCGAGAAACATGTGAGT 92
DB 13 GCCCGCGAGAACATGTGAGT 33

RESULT 64
US-09-345-294-9
Sequence 9, Application US/09345294
Patent No. 6387619
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,294
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-345-294-9

Query Match 15.7%; Score 14.6; DB 4; Length 40;
Best Local Similarity 69.0%; Pred. No. 4.9e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 63 GACTGCGGCGCTCCAGAAACATGTGAGG 91
DB 6 GACTGCTGCTCCAGAAACATGTGAGG 34

RESULT 65
US-08-832-985-74/c
Sequence 74, Application US/08832985
Patent No. 6057098
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Walkers, Gunars
TITLE OF INVENTION: POLYVALENT DISPLAY LIBRARIES
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,985
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 014907-001000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-832-985-74

Query Match 15.7%; Score 14.6; DB 3; Length 43;
Best Local Similarity 62.2%; Pred. No. 5.1e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 37 CCTTGCTTCAACACTATCGAATGTGACTGTGCGGC 73
DB 39 CCTGGCTTATCAAAATATCGCGCAATGCTGTGCGGC 3

RESULT 66
US-09-410-903-55/c
Sequence 55, Application US/09410903
Patent No. 6420113
GENERAL INFORMATION:
APPLICANT: Buechler, Joe

APPLICANT: ValKirs, Gunars
APPLICANT: Gray, Jeff
TITLE OF INVENTION: Biosite Diagnostics Inc.
FILE REFERENCE: 014907-002700US
CURRENT APPLICATION NUMBER: US/09/410,903
PRIOR FILING DATE: 1999-10-02
PRIOR APPLICATION NUMBER: US 08/832,985
PRIOR FILING DATE: 1997-04-04
PRIOR APPLICATION NUMBER: US 08/835,159
PRIOR FILING DATE: 1997-04-04
PRIOR APPLICATION NUMBER: WO PCT/US98/06704
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55
LENGTH: 43
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligo 55
US-09-410-903-55

Query Match 15.7%; Score 14.6; DB 4; Length 43;
Best Local Similarity 62.2%; Pred. No. 5.1e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY - 37 CCTGGTTTCACACTATCGAATGTGACTGTGGGC 73
DB 39 CCTGGTTTCACACTATCGCCATGCTGTGGGC 3

RESULT 67
US-08-229-279-4/c
Sequence 4, Application US/08229279
Patent No. 5648211
GENERAL INFORMATION:
APPLICANT: Fraiser, Melinda S.
APPLICANT: Spargo, Catherine A.
APPLICANT: Walker, George T.
APPLICANT: Van Cleve, Mark
APPLICANT: Wright, David J.
TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
TITLE OF INVENTION: THERMOPHILIC ENZYMES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESS: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,279
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-2961
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-229-279-4
Query Match 15.7%; Score 14.6; DB 1; Length 45;
Best Local Similarity 62.2%; Pred. No. 5.2e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 34 ATGCCTGGTTTCACACTATCGAATGTGACTGTGG 70
DB 39 ATGCCTGGTTTCACACTATCGCCATGCTGTGG 3

RESULT 68
US-08-701-269-4/c
Sequence 4, Application US/08701269
Patent No. 5744311
GENERAL INFORMATION:
APPLICANT: Fraiser, Melinda S.
APPLICANT: Spargo, Catherine A.
APPLICANT: Walker, George T.
APPLICANT: Van Cleve, Mark
APPLICANT: Wright, David J.
TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
TITLE OF INVENTION: THERMOPHILIC ENZYMES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESS: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,269
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-2961
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-701-269-4
Query Match 15.7%; Score 14.6; DB 1; Length 45;
Best Local Similarity 62.2%; Pred. No. 5.2e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 34 ATGCCTGGTTTCACACTATCGAATGTGACTGTGG 70
DB 39 ATGCCTGGTTTCACACTATCGCCATGCTGTGG 3

RESULT 69
US-09-605-785-782
Sequence 782, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiaqichun
APPLICANT: Dillon, Davin C.

```

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Mang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: PASTESEQ for Windows Version 3.0
; SEQ ID NO 782
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-605-785-782

Query Match      15.7%; Score 14.6; DB 4; Length 45;
Best Local Similarity 57.8%; Pred. No. 5.2e+03;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      31 ACAATGCTTGGTTCAACACTATCGAATGTGACTGCGGCGCT 75
Db      1 AGAATGCTACCGCTGCTGCAGTGTGGAACGTGTGGGTGTCT 45

RESULT 70
US-08-184-009-187
; Sequence 187, Application US/08184009
; Patent No. 5833975
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,009
; FILING DATE: 19-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-184-009-187

; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-184-009-187

Query Match      15.7%; Score 14.6; DB 2; Length 47;
Best Local Similarity 57.8%; Pred. No. 5.3e+03;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      35 TGCCCTGGTTCAACACTATCGAATGTGACTGCGGCGCTCCAG 79
Db      3 TGGTGTGTAGTCTCTCTCTAAATAATGTGCTGCAGAGCCTGCTG 47

RESULT 71
US-08-458-356-187
; Sequence 187, Application US/08458356
; Patent No. 5942235
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,356
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/184,009
; FILING DATE: 19-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-458-356-187

; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-184-009-187

Query Match      15.7%; Score 14.6; DB 2; Length 47;
Best Local Similarity 57.8%; Pred. No. 5.3e+03;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      35 TGCCCTGGTTCAACACTATCGAATGTGACTGCGGCGCTCCAG 79
Db      3 TGGTGTGTAGTCTCTCTCTAAATAATGTGCTGCAGAGCCTGCTG 47

RESULT 72
US-08-460-736-187
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; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-184-009-187

Query Match      15.7%; Score 14.6; DB 2; Length 47;
Best Local Similarity 57.8%; Pred. No. 5.3e+03;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      35 TGCCCTGGTTCAACACTATCGAATGTGACTGCGGCGCTCCAG 79
Db      3 TGGTGTGTAGTCTCTCTCTAAATAATGTGCTGCAGAGCCTGCTG 47

RESULT 72
US-08-460-736-187
```

Sequence 187, Application US/08460736
Patent No. 6265189
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Paoletti, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTWS
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-460-736-187

Query Match 15.7%; Score 14.6; DB 4; Length 47;
Best Local Similarity 57.8%; Pred. No. 5.3e+03;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 35 TGCCCTGCTTCAACTATCGGATGTGACTGTGGGCGCTCCAG 79
DB 3 TGGTGTGTAGTCTCTCTAATAATGGCGTGAAGAGCCTGCTG 47

RESULT 73
US-08-093-453B-7
Sequence 7, Application US/08093453B
Patent No. 5439814
GENERAL INFORMATION:
APPLICANT: Frey, Terry K.
APPLICANT: Dominguez, Geraldina
APPLICANT: Wang, Chin-Yen
TITLE OF INVENTION: Modified Infectious Rubella Virus
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jamie L. Greene, Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: United States
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh

OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,453B
FILING DATE: 19 JUL 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/722,334
FILING DATE: 28 JUN 1991
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 07362-0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404.818-3799
TELEFAX: 404.818-3700
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rubella virus
STRAIN: Thertien
US-08-093-453B-7

Query Match 15.7%; Score 14.6; DB 1; Length 48;
Best Local Similarity 69.0%; Pred. No. 5.4e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 48 ACACTATCGAATGTGACTGTGGGCGCTC 76
DB 20 ACACTATGACATGAGACTATCGGACTTC 48

RESULT 74
US-08-459-041A-4
Sequence 4, Application US/08459041A
Patent No. 5663065
GENERAL INFORMATION:
APPLICANT: Frey, Terry K.
APPLICANT: Dominguez, Geraldina
APPLICANT: Wang, Chin-Yen
TITLE OF INVENTION: DNA Encoding Infectious Rubella Virus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,041A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 07362-0102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 4:

CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,637
FILING DATE: 10-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/579,233
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/152,313
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hall, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/146001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-038-637-135

Query Match 15.5%; Score 14.4; DB 4; Length 20;
Best Local Similarity .93.8%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 GCCTGGGTGACATGC 37
DB 2 GCCTGGGTGACAAAGC 17

RESULT 78
US-07-613-083B-2
Sequence 2, Application US/07613083B
Patent No. 5340727
GENERAL INFORMATION:
APPLICANT: Ruggeri, Zaverio M.
APPLICANT: Ware, Jerry, inventors
APPLICANT: on behalf of Scripps Clinic and Research
APPLICANT: Foundation
TITLE OF INVENTION: GPIIb Fragments and Recombinant
TITLE OF INVENTION: DNA Expression Vectors
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scripps Clinic and Research
STREET: 10666 No. 5340727th Torrey Pines Road
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2 Mb
COMPUTER: AST Bravo IBM PC comp. (386SX)
OPERATING SYSTEM: MS DOS version 3.2
SOFTWARE: WordPerfect 5.1 conv. to ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/613,083B
FILING DATE: 19911114
CLASSIFICATION: 435
PRIOR APPLICATION DATA: This appl. is a c-i-p of
APPLICATION NUMBER: U.S. 07/470,674

FILING DATE: 04-Jan-1990
ATTORNEY/AGENT INFORMATION:
NAME: Batton, Alexis
REGISTRATION NUMBER: 22,702
REFERENCE/DOCKET NUMBER: P16,569-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 923-4466
TELEFAX: (215) 923-2189
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-07-613-083B-2

Query Match 15.5%; Score 14.4; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 57 GAATGTACTGTGCGCCTCCAGA 80
DB 1 GAATGTGACAGCGCTGCTCCAGA 24

RESULT 79
US-08-474-021-2/C
Sequence 2, Application US/08474021
Patent No. 5650282
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Leppert, Mark F.
APPLICANT: Morris, Colleen A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SUPRAVALVULAR
TITLE OF INVENTION: AORTIC STENOSIS AND WILLIAMS SYNDROME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Ave., N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,021
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/041,576
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 19780-105509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4800
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-474-021-2

Query Match 15.5%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 AATGTGACTGTCGGGCTCCAGAA 81
DB 31 AACTGGCTCCAGGCTCCAGAA 8

RESULT 80

US-08-474-020A-2/C
; Sequence 2, Application US/08474020A
; Patent No. 5840489

GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Leppert, Mark F.
APPLICANT: Morris, Colleen A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SUPRAVALVULAR
TITLE OF INVENTION: AORTIC STENOSIS AND WILLIAMS SYNDROME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Ave., N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,020A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/041,576
FILING DATE: 05-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 19780-105509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4800
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-474-020A-2

Query Match 15.5%; Score 14.4; DB 2; Length 32;
Best Local Similarity 75.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 AATGTGACTGTCGGGCTCCAGAA 81
DB 31 AACTGGCTCCAGGCTCCAGAA 8

RESULT 81

PCT-US94-03426-2/C
; Sequence 2, Application PC/TUS9403426
; GENERAL INFORMATION:

APPLICANT: Keating, Mark T.
APPLICANT: Leppert, Mark F.
APPLICANT: Morris, Colleen A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SUPRAVALVULAR
TITLE OF INVENTION: STENOSIS AND WILLIAMS SYNDROME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Ave., N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03426
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 19780-105509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4800
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US94-03426-2

Query Match 15.5%; Score 14.4; DB 5; Length 32;
Best Local Similarity 75.0%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 AATGTGACTGTCGGGCTCCAGAA 81
DB 31 AACTGGCTCCAGGCTCCAGAA 8

RESULT 82

US-08-840-466A-10/C
; Sequence 10, Application US/08840466A
; Patent No. 6261561
GENERAL INFORMATION:
APPLICANT: Stewart, C. Neal
APPLICANT: Wicke, Marian L.
APPLICANT: O'Brien, Allison D.
APPLICANT: Wachtel, Marian R.

TITLE OF INVENTION: Method Of Stimulating An Immune Response

By Administration Of Host Organisms That Express Intimin
Alone Or As A Fusion Protein With One Or More Other
Antigens.

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,466A
FILING DATE: 18-Apr-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Boone, Laurel S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-840-466A-10
Query Match 15.5%; Score 14.4; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 36 GCCTGGTTTCAACACTGCGAA 59
|||||
DB 25 GCCTGGTTGATCAGATCCGTA 2
RESULT 83
US-09-696-188B-10/c
Sequence 10, Application US/09696188B
Patent No. 6406885
GENERAL INFORMATION:
APPLICANT: Stewart, C. Neal
McKee, Marian L.
O'Brien, Alison D.
Machtel, Marian R.
TITLE OF INVENTION: Method of Stimulating An Immune Response
By Administration Of Host Organisms That Express Intimin
Alone Or As A Fusion Protein With One Or More Other
Antigens.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/696,188B
FILING DATE: 26-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/840,466
FILING DATE: 1997-04-18
ATTORNEY/AGENT INFORMATION:
NAME: Boone, Laurel S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-696-188B-10
Query Match 15.5%; Score 14.4; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 36 GCCTGGTTTCAACACTGCGAA 59
|||||
DB 25 GCCTGGTTGATCAGATCCGTA 2
RESULT 84
US-09-375-318-6
Sequence 6, Application US/09375318
Patent No. 6468791
GENERAL INFORMATION:
APPLICANT: Tanzil, Rudolph E.
Schellenberg, Gerard D.
Masco, Wilma
Levy-Lahad, Ephrat
Bird, Thomas D.
Galas, David J.
TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BEERY LLP
STREET: 701 Fifth Ave, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,318
FILING DATE: 16-Aug-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Verma, James M.
REGISTRATION NUMBER: 33,287
REFERENCE/DOCKET NUMBER: 920010.571c1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-375-318-6
Query Match 15.5%; Score 14.4; DB 4; Length 39;
Best Local Similarity 93.8%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 22 GCCTGGTGAACATGC 37
|||||

Db .23 GCCTGGGTGACAAAGC 38

RESULT 85

US-08-301-722A-6/c

Sequence 6, Application US/08301722A

Patent No. 5756307

GENERAL INFORMATION:

APPLICANT: Uhl, George R.

APPLICANT: Vandenberg, David

APPLICANT: Persico, Antonio

TITLE OF INVENTION: SEQUENCE OF HUMAN DOPAMINE TRANSPORTER

TITLE OF INVENTION: CDNA

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22040-3487

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/301,722A

FILING DATE: 07-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1173-406P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8050

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

HYPOTHEICAL: YES

ANTI-SENSE: NO

FEATURE:

NAME/KEY:

LOCATION: 1..40

OTHER INFORMATION: /label= consensus

OTHER INFORMATION: /note="consensus sequence of VNTN element in 3'

OTHER INFORMATION: untranscribed region of HMDT cDNA"

US-08-301-722A-6

Query Match 15.5%; Score 14.4; DB 1; Length 40;

Best Local Similarity 75.0%; Pred. No. 6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TGGGACACATTCATTCCTGGG 28

Db 39 TGGGGCCCTGCATTCCTGGG 16

RESULT 86

US-08-687-559-19/c

Sequence 19, Application US/08687559

Patent No. 5955647

GENERAL INFORMATION:

APPLICANT: Fitch, John H.

APPLICANT: Beachy, Roger N.

TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO

TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,559

FILING DATE: No. 5955647ember 18, 1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01467

FILING DATE: 03-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Leairn, June M.

REGISTRATION NUMBER: 31,238

REFERENCE/DOCKET NUMBER: 07302/011001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-08-687-559-19

Query Match 15.5%; Score 14.4; DB 2; Length 44;

Best Local Similarity 75.0%; Pred. No. 6.2e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 68 TCGGGCTCGCAAAACATTTAGG 91

Db 37 TTGGACCTCTAGATTCATTTAGG 14

RESULT 87

US-08-145-704-44

Sequence 44, Application US/08145704

Patent No. 5567604

GENERAL INFORMATION:

APPLICANT: Rando, Robert F.

APPLICANT: Fennwald, Susan

APPLICANT: Zendegeul, Joseph G.

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Oligonucleotides

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski

STREET: 1301 McKinney, Suite 5100

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77010-3095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/145,704

FILING DATE: 28-OCT-1993

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

RESULT 90

US-09-017-974-44

; Sequence 44, Application US/09017974

; Patent No. 6288042

; GENERAL INFORMATION:

; APPLICANT: Rando, Robert F.

; APPLICANT: Ojwang, Joshua O.

; APPLICANT: Hogan, Michael E.

; APPLICANT: Wallace, Thomas L.

; APPLICANT: Cossam, Paul A.

; TITLE OF INVENTION: Anti-Viral Guanosine-Rich

; TITLE OF INVENTION: Tetrad Forming Oligonucleotides

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Conley, Rose & Tayon, P.C.

; STREET: 600 Travis, Suite 1800

; CITY: Houston

; STATE: Texas

; COUNTRY: U.S.A.

; ZIP: 77002-2912

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word 97 (saved as .txt file)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/017,974

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 60/037,374

; FILING DATE: 04-FEB-97

; APPLICATION NUMBER:

; FILING DATE: 09-DEC-97

; ATTORNEY/AGENT INFORMATION:

; NAME: McDaniel, C. Steven

; REGISTRATION NUMBER: 33,962

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713/238-8010

; TELEFAX: 713/238-8008

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-09-017-974-44

Query Match 15.5%; Score 14.4; DB 4; Length 47;

Best Local Similarity 65.6%; Pred. No. 6.4e+03;

Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGAATGACTGTCGGCC 74
Db 6 TTGGGAACCTTGGAACCTGACTGACTGCGCC 37

RESULT 91

US-08-682-255A-44

; Sequence 44, Application US/08682255A

; Patent No. 6323185

; GENERAL INFORMATION:

; APPLICANT: Rando, Robert F.

; APPLICANT: Fennwald, Susan

; APPLICANT: Ojwang, Joshua O.

; APPLICANT: Hogan, Michael E.

; APPLICANT: Pommler, Eves

; APPLICANT: Mazunder, Abhijit

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Oligonucleotides

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1850

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS Windows 95

SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,255A

FILING DATE: 17-JULY-1996

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/535,168

FILING DATE: 23-OCT-95

APPLICATION NUMBER: 60/001,505

FILING DATE: 19-JULY-95

APPLICATION NUMBER: 60/014,007

FILING DATE: 25-MARCH-96

APPLICATION NUMBER: 60/013,688

FILING DATE: 19-MARCH-96

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 23-APRIL-96

ATTORNEY/AGENT INFORMATION:

NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/238-8010

TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-682-255A-44

Query Match 15.5%; Score 14.4; DB 4; Length 47;

Best Local Similarity 65.6%; Pred. No. 6.4e+03;

Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGAATGACTGTCGGCC 74
Db 6 TTGGGAACCTTGGAACCTGACTGACTGCGCC 37

RESULT 92

US-09-429-130-44

; Sequence 44, Application US/09429130

; Patent No. 6355785

; GENERAL INFORMATION:

; APPLICANT: Rando, Robert F.

; APPLICANT: Fennwald, Susan

; APPLICANT: Ojwang, Joshua O.

; APPLICANT: Hogan, Michael E.

; APPLICANT: Pommler, Eves

; APPLICANT: Mazunder, Abhijit

; TITLE OF INVENTION: Anti-Viral Guanosine-Rich

; NUMBER OF SEQUENCES: 87

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Oligonucleotides

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1850

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS Windows 95

SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,255A

FILING DATE: 17-JULY-1996

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/535,168

FILING DATE: 23-OCT-95

APPLICATION NUMBER: 60/001,505

FILING DATE: 19-JULY-95

APPLICATION NUMBER: 60/014,007

FILING DATE: 25-MARCH-96

APPLICATION NUMBER: 60/013,688

FILING DATE: 19-MARCH-96

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 23-APRIL-96

ATTORNEY/AGENT INFORMATION:

NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/238-8010

TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-682-255A-44

Sun Jul 6 13:51:01 2003

us-09-843-377-3_1000_1092.szm50.rni

Page 42

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96

ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-429-130-44

Query Match      15.5%; Score 14.4; DB 4; Length 47;
Best Local Similarity 65.6%; Pred. No. 6,4e+03;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

          43 TTTCACACTATGCGATGTGGTGGGCC 74
            ||| | ||| ||||| ||||| |||||
Db       6 TTGGCAAACTTGGAAGCTGACTGAGCC 37

RESULT 93
PCT-US96-11786-44
Sequence 44, Application PC/TUS9611786
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendegeul, Joseph G.
APPLICANT: O'wang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Pomlier, Yves
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
```

```

1 ADDRESS: Conley, Rose & Tayon, P.C.
2 STREET: 600 Travis, Suite 1850
3 CITY: Houston
4 STATE: Texas
5 COUNTRY: U.S.A.
6 ZIP: 77002-2912
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patent Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: PCT/US96/11786
15 FILING DATE: 17-JULY-1996
16
17 CLASSIFICATION:
18 PRIORITY APPLICATION DATA:
19 APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
20 APPLICATION NUMBER: 60/015,714; 60/016,271
21 FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
22 FILING DATE: APRIL-96; 17-APRIL-96
23 ATTORNEY/AGENT INFORMATION:
24 NAME: McDaniel, C. Steven
25 REGISTRATION NUMBER: 33,962
26 REFERENCE/DOCKET NUMBER: 1472-06214
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 713/238-8010
29 TELEFAX: 713/238-8008
30 INFORMATION FOR SEQ ID NO: 44:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 47 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: DNA (genomic)
37 PCT-US96-11786-44
38
39 Query Match 15.5%; Score 14.4; DB 5; Length 47;
40 Best Local Similarity 65.6%; Pred. No. 6.4e+03;
41 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
42
43 Oy 43 TTTCACACTATCGAATGACTGTCGGGCC 74
44 11 11 11 11 11 11 11 11 11 11
45 Db 6 TTGGGAACCTTGGAACCTGACTGACTGCC 37
46
47 RESULT 94
48 US-08-916-5768-26/C
49 Sequence 26, Application US/08916576B
50 Patent No. 6171816
51 GENERAL INFORMATION:
52 APPLICANT: YU, GUO-LIANG
53 APPLICANT: DILON, PATRICK J.
54 APPLICANT: EBNER, REINHARD
55 APPLICANT: ENDRESS, GREGORY A.
56 TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
57 NUMBER OF SEQUENCES: 45
58 CORRESPONDENCE ADDRESS:
59 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
60 STREET: 1100 NEW YORK AVENUE, SUITE 600
61 CITY: WASHINGTON
62 STATE: DC
63 COUNTRY: US
64 ZIP: 20005-3934
65
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC-DOS/MS-DOS
70 SOFTWARE: Patent Release #1.0, Version #1.30
71 CURRENT APPLICATION DATA:
72 APPLICATION NUMBER: US/08/916,576B
73 FILING DATE:
74 CLASSIFICATION: 536
75 PRIORITY APPLICATION DATA:

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ORGANISM: Aequorea victoria
US-09-049-475-7

Query Match      15.3%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

QY      1 GAGCTGGAGCAGTCACATT 19
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Db      1 GAGCTGGAGCAGTCACAGT 19

RESULT 96
US-08-513-974B-81/c
: Sequence 81, Application US/08513974B
: Patent No. 6114139
:
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohcaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-81

Query Match 15.3%; Score 14.2; DB 3; Length 27;
Best Local Similarity 84.2%; Pred. No. 6e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 65 CTGTCGGGCTCCAGAAA 83
DB 26 CTGTAGGCATCATATAA 8

RESULT 97
US-08-340-011-16
Sequence 16, Application US/08340011
Patent No. 578755
GENERAL INFORMATION:
APPLICANT: Alltalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-340-011-16

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Best Local Similarity 84.2%; Pred. No. 6.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 GGGAGCACTCCATTCGCC 24
DB 2 GGGATCCTCCATTCGCC 20

RESULT 98
US-08-901-710-16
Sequence 16, Application US/08901710
Patent No. 6107046
GENERAL INFORMATION:
APPLICANT: Alltalo, Karl
APPLICANT: Apetlikova, Olga
APPLICANT: Pajusola, Katri
APPLICANT: Armstrong, Elna
APPLICANT: Korhonen, Jaana
APPLICANT: Kalpainen, Arja
APPLICANT: Mälikäinen, Marja-Terttu
TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,710
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,754
FILING DATE: 09-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33824
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-901-710-16

Query Match 15.3%; Score 14.2; DB 3; Length 28;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGGAGCACTCCATTCGCC 24
DB 2 GGGATCCTCCATTCGCC 20


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RESULT 99
US-08-331-081B-16/c
; Sequence 16, Application US/08331081B
; Patent No. 5998697
; GENERAL INFORMATION:
; APPLICANT: Devlin, Robert H.
; TITLE OF INVENTION: Transgenic Fish and Vectors Therefor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: McFadden, Fincham
; STREET: 225 Metcalfe Street, Suite 606
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K2P 1P9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC or Compatibles
; OPERATING SYSTEM: PC Dos 5.0
; SOFTWARE: Wordperfect 5.1 (Patseq.txt)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,081B
; FILING DATE: October 20, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Canada 2,126,138
; FILING DATE: June 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fincham, H. Ian
; REGISTRATION NUMBER: 26,375
; REFERENCE/DOCKET NUMBER: 5478-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 234-1907
; TELEFAX: (613) 234-5233
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single (part of double)
; TOPOLOGY: linear
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US-08-331-081B-16

Query Match      15.3%; Score 14.2; DB 2; Length 29;
Best Local Similarity 70.4%; Pred. No. 6.2e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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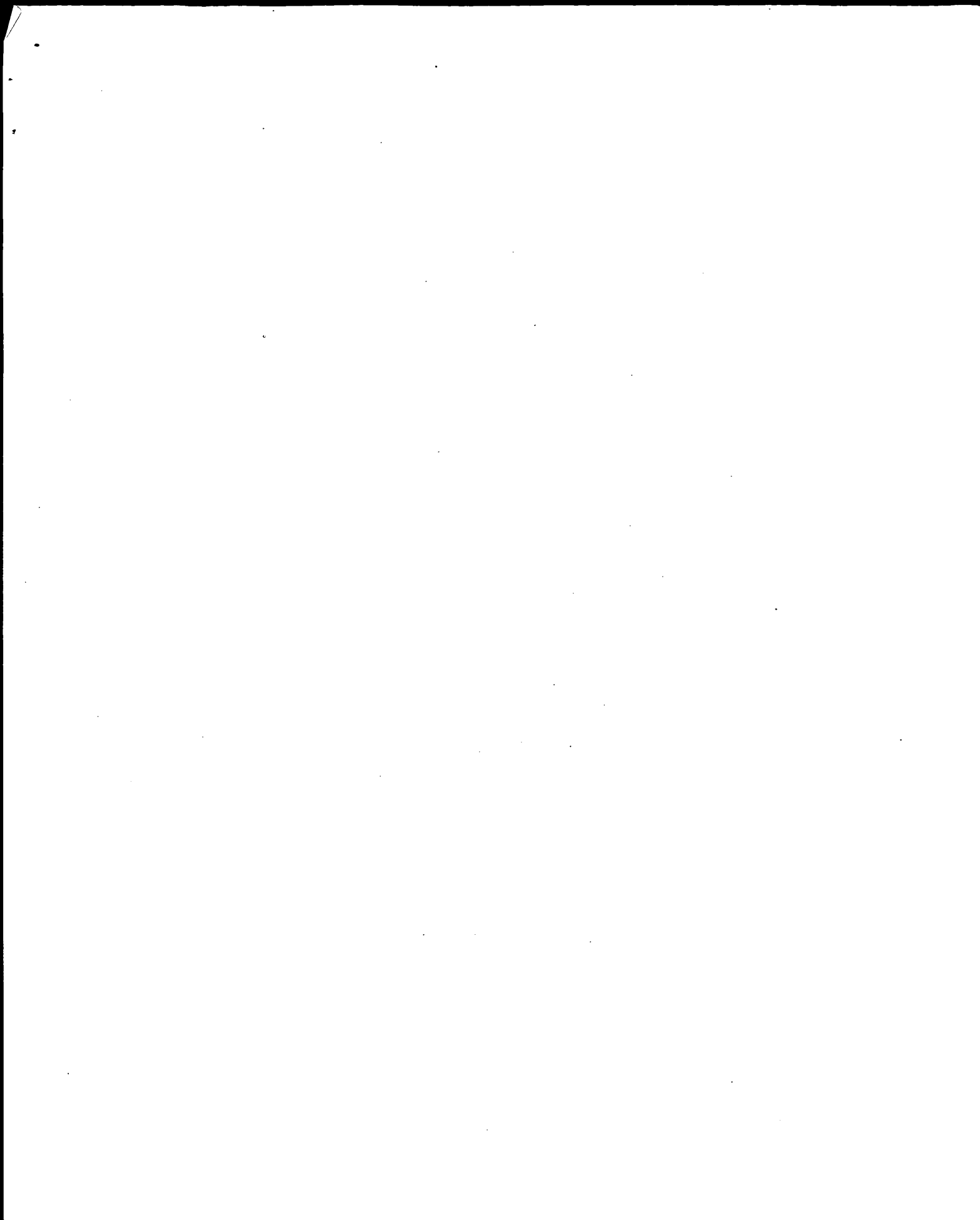
RESULT 100
US-08-627-907A-8
; Sequence 8, Application US/08627907A
; Patent No. 6060302
; GENERAL INFORMATION:
; APPLICANT: HIRANO, Naoto
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,907A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-238402
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01572
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "mutagenic primer"
;
US-08-627-907A-8

Query Match      15.3%; Score 14.2; DB 3; Length 30;
Best Local Similarity 70.4%; Pred. No. 6.3e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db      4 CCTTGTTTCGTCACCTCAAGATGCG 30

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Job time : 80 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 10:01:04 ; Search time 1357 Seconds
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Title: US-09-843-377-3_COPY_1000_1092

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: em_estlin:*
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12: gb_est3:*
13: gb_est4:*
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26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18.2	19.6	49	17	AT758166
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56	14.4	15.5	50	9	AU106860
57	14.4	15.5	50	10	AA936264
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AV833659 AV833659
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101	13.8	14.8	50	9	AU102306	AU102306 AU102306	C	174	13.2	14.2	34	17	BH789679	BH789679 SALK_0444
102	13.8	14.8	50	9	AU102884	AU102884 AU102884	C	175	13.2	14.2	35	9	AI801185	AI801185 c073h04..x
103	13.8	14.8	50	9	AU105745	AU105745 AU105745	C	176	13.2	14.2	35	14	U44207	U44207 ENU44207..AS
104	13.8	14.8	50	9	AU106025	AU106025 AU106025	C	177	13.2	14.2	37	17	AZ512936	AZ512936 1M0358N15
105	13.8	14.8	50	17	AO025065	AO025065 BP(3)0339	C	178	13.2	14.2	39	13	BI653065	BI653065 603300775
106	13.6	14.6	22	17	AA814281	AA814281 2M0082L04	C	179	13.2	14.2	39	14	D19135	D19135 MWSG501351
107	13.6	14.6	28	17	AA310043	AA310043 1M0018K09	C	180	13.2	14.2	39	17	AA372602	AA372602 1M0124J02
108	13.6	14.6	34	10	BE303175	BE303175 601099124	C	181	13.2	14.2	39	17	BH863618	BH863618 SALK_0942
109	13.6	14.6	34	14	T89869	T89869 yd99e12..s1	C	182	13.2	14.2	40	10	AA834352	AA834352 c073h04..x
110	13.6	14.6	34	14	AZ474616	AZ474616 1M0292B14	C	183	13.2	14.2	41	17	AE511081	AE511081 1M0350Z00
111	13.6	14.6	36	14	R85453	R85453 YQ26904..s1	C	184	13.2	14.2	41	17	N21357	N21357 yx0e11..s1
112	13.6	14.6	37	9	AA680722	AA680722 1MfTAm022	C	185	13.2	14.2	43	9	BH852373	BH852373 SALK_0745
113	13.6	14.6	40	9	AU104082	AU104082 c052b05..x	C	186	13.2	14.2	43	17	AI000245	AI000245 c004e01..s
114	13.6	14.6	40	14	W96287	W96287 z642a10..r1	C	187	13.2	14.2	44	9	AA319659	AA319659 1M0039E04
115	13.6	14.6	41	17	AA832243	AA832243 2M0156M15	C	188	13.2	14.2	45	9	AI494250	AI494250 qy98a01..x
116	13.6	14.6	41	17	BH789196	BH789196 SALK_0009	C	189	13.2	14.2	45	9	AA009110	AA009110 mq92a09..r
117	13.6	14.6	43	9	AA878695	AA878695 c023c05..s	C	190	13.2	14.2	46	9	AI441323	AI441323 s852h10..y
118	13.6	14.6	43	9	AI786712	AI786712 u156b03..x	C	191	13.2	14.2	46	9	AA428172	AA428172 z550006..x
119	13.6	14.6	43	9	BI690746	BI690746 603314363	C	192	13.2	14.2	46	17	AA817952	AA817952 2M0087008
120	13.6	14.6	43	13	R07988	R07988 yf16f09..s1	C	193	13.2	14.2	46	17	BH846813	BH846813 SALK_0105
121	13.6	14.6	43	14	AI937592	AI937592 wP81d11..x	C	194	13.2	14.2	47	13	BI082347	BI082347 602877544
122	13.6	14.6	46	9	AA832553	AA832553 AV832553	C	195	13.2	14.2	47	17	AA761099	AA761099 1M0555D13
123	13.6	14.6	46	10	AA808188	AA808188 2M0077C14	C	196	13.2	14.2	47	17	AZ768567	AZ768567 SALK_0901
124	13.6	14.6	46	17	AA834972	AA834972 2M0117M19	C	197	13.2	14.2	47	17	BH862606	BH862606 1M0568D05
125	13.6	14.6	46	17	AA834972	AA834972 2M0117M19	C	198	13.2	14.2	47	17	AA631597	AA631597 1M0485A24
126	13.6	14.6	46	17	BH851050	BH851050 SALK_0723	C	199	13.2	14.2	48	17	AI119820	AI119820 uc21b12..r
127	13.6	14.6	47	9	AL799469	AL799469 AL799469	C	200	13.2	14.2	48	9	AI167613	AI167613 w195e10..x
128	13.6	14.6	48	12	BF506898	BF506898 10952P-16	C	201	13.2	14.2	49	9	AA428326	AA428326 zw18e03..s
129	13.6	14.6	50	9	AU105569	AU105569 AU105569	C	202	13.2	14.2	49	13	BM183028	BM183028 fw29e09..y
130	13.6	14.6	50	9	AU105800	AU105800 AU105800	C	203	13.2	14.2	49	13	CO1053	CO1053 HMG5000735
131	13.6	14.6	50	9	AU106865	AU106865 AU106865	C	204	13.2	14.2	49	14	CO1053	CO1053 HMG5000735
132	13.6	14.6	50	12	BG370398	BG370398 na133a04..	C	205	13.2	14.2	49	17	AZ586447	AZ586447 1M0392B22
133	13.6	14.6	50	17	AA837772	AA837772 AST-T32B0	C	206	13.2	14.2	50	9	AU102454	AU102454 AU102454
134	13.6	14.6	50	17	AA883279	AA883279 e114d10..s	C	207	13.2	14.2	50	9	AU102455	AU102455 AU102455
135	13.4	14.4	28	17	BH813063	BH813063 SALK_0636	C	208	13.2	14.2	50	9	AU102457	AU102457 AU102457
136	13.4	14.4	29	17	AZ494908	AZ494908 1M0330A04	C	209	13.2	14.2	50	9	AU103446	AU103446 AU103446
137	13.4	14.4	32	17	AZ821174	AZ821174 2M0093M16	C	210	13.2	14.2	50	9	AU103453	AU103453 AU103453
138	13.4	14.4	35	17	AZ822760	AZ822760 2M0096M16	C	211	13.2	14.2	50	9	AU103461	AU103461 AU103461
139	13.4	14.4	36	14	R60498	R60498 yh13h12..s1	C	212	13.2	14.2	50	9	AU103470	AU103470 AU103470
140	13.4	14.4	37	10	AV955285	AV955285 AV955285	C	213	13.2	14.2	50	9	AU103471	AU103471 AU103471
141	13.4	14.4	37	17	AA958064	AA958064 2M0225L08	C	214	13.2	14.2	50	9	AU103472	AU103472 AU103472
142	13.4	14.4	39	10	AV954296	AV954296 AV954296	C	215	13.2	14.2	50	9	AU103614	AU103614 AU103614
143	13.4	14.4	40	17	AZ785563	AZ785563 2M0029I06	C	216	13.2	14.2	50	9	AU104317	AU104317 AU104317
144	13.4	14.4	41	17	AZ773828	AZ773828 2M0001P06	C	217	13.2	14.2	50	9	AU104401	AU104401 AU104401
145	13.4	14.4	43	17	AI627640	AI627640 ty81a12..x	C	218	13.2	14.2	50	9	AU104739	AU104739 AU104739
146	13.4	14.4	43	17	AZ588360	AZ588360 1M0396E09	C	219	13.2	14.2	50	9	AU106009	AU106009 AU106009
147	13.4	14.4	43	17	BH811442	BH811442 SALK_0586	C	220	13.2	14.2	50	9	AU107397	AU107397 AU107397
148	13.4	14.4	43	17	AA688973	AA688973 ak24e07..s	C	221	13.2	14.2	50	10	AV971298	AV971298 AV971298
149	13.4	14.4	46	17	BH851120	BH851120 SALK_0724	C	222	13.2	14.2	28	9	BI738814	BI738814 603362674
150	13.4	14.4	46	17	BH865380	BH865380 SALK_0983	C	223	13.2	14.2	31	13	BI522142	BI522142 603081524
151	13.4	14.4	47	13	BJ084126	BJ084126 BJ084126	C	224	13.2	14.2	31	17	AA625018	AA625018 1M0464I04
152	13.4	14.4	47	13	BJ084126	BJ084126 BJ084126	C	225	13.2	14.2	31	17	AA625018	AA625018 1M0464I04

C 226	13	14.0	32	14	R56853	R56853 Y104903.s1	299	12.8	13.8	40	17	A257561	A257561 AST-T32B0
C 227	13	14.0	33	17	A2841697	A2841697 2M0139A20	C 300	12.8	13.8	40	17	A2779365	A2779365 2M0015810
C 228	13	14.0	34	9	A1218270	A1218270 qb28f05.x	C 301	12.8	13.8	40	17	BH63408	BH63408 SALK_0938
C 229	13	14.0	34	9	A1378501	A1378501 tcs6h07.x	C 302	12.8	13.8	40	17	AL756146	AL756146 Arabidops
C 230	13	14.0	36	9	AL667129	AL667129 AL667129	C 303	12.8	13.8	41	17	AA019796	AA019796 z62h02.x
C 231	13	14.0	36	17	AL667129	AL667129 AL667129	C 304	12.8	13.8	41	17	AA976917	AA976917 ocq3h04.s
C 232	13	14.0	36	17	AL789802	AL789802 AL789802	C 305	12.8	13.8	41	14	H98601	H98601 yx16b01.s1
C 233	13	14.0	37	13	BJ054485	BJ054485 BJ054485	C 306	12.8	13.8	42	10	AL801104	AL801104 SMY25C4U
C 234	13	14.0	38	17	A2621238	A2621238 1M0454A22	C 307	12.8	13.8	42	17	TA131C01P	TA131C01P
C 235	13	14.0	38	17	A2738399	A2738399 2M0001A18	C 308	12.8	13.8	42	17	AA433612	AA433612 ve36b01.x
C 236	13	14.0	39	10	A2863007	A2863007 2M010N23	C 309	12.8	13.8	43	10	AA534781	AA534781 n816s01.s
C 237	13	14.0	39	14	H57425	H57425 Y13a11.s1	C 310	12.8	13.8	43	10	AA834377	AA834377 AV834377
C 238	13	14.0	39	14	H57425	H57425 Y13a11.s1	C 311	12.8	13.8	43	10	H92514	H92514 y866h10.s1
C 239	13	14.0	39	17	A2836522	A2836522 2M0134F22	C 312	12.8	13.8	43	17	A2488436	A2488436 1M0318012
C 240	13	14.0	40	9	AL154170	AL154170 ud78h11.x	C 313	12.8	13.8	44	14	NA7451	NA7451 y99c010.s1
C 241	13	14.0	40	9	AL1900611	AL1900611 sc31f07.y	C 314	12.8	13.8	44	17	A2488436	A2488436 1M0318012
C 242	13	14.0	40	9	AU255509	AU255509 AU255509	C 315	12.8	13.8	44	14	NA7451	NA7451 y99c010.s1
C 243	13	14.0	40	17	A2595177	A2595177 1M0407E07	C 316	12.8	13.8	44	17	A2488436	A2488436 1M0318012
C 244	13	14.0	40	17	A2664762	A2664762 1M0545P18	C 317	12.8	13.8	44	17	A2488436	A2488436 1M0318012
C 245	13	14.0	41	17	A2778876	A2778876 2M0014D03	C 318	12.8	13.8	45	9	AA499333	AA499333 v185s02.x
C 246	13	14.0	42	13	BJ054561	BJ054561 BJ054561	C 319	12.8	13.8	45	17	A2820873	A2820873 2M0093F23
C 247	13	14.0	42	13	BJ054561	BJ054561 BJ054561	C 320	12.8	13.8	45	17	BH790849	BH790849 SALK_0580
C 248	13	14.0	42	17	TA57019	TA57019 ya84d02.s2	C 321	12.8	13.8	46	9	AU008835	AU008835
C 249	13	14.0	42	17	A2630926	A2630926 1M0485C06	C 322	12.8	13.8	46	17	A2696573	A2696573 2M0242E21
C 250	13	14.0	44	17	A2441861	A2441861 1M0234D18	C 323	12.8	13.8	46	17	BH846317	BH846317 SALK_0072
C 251	13	14.0	44	17	A2591573	A2591573 1M0401E15	C 324	12.8	13.8	47	17	CNS07FA0	CNS07FA0
C 252	13	14.0	44	17	A2591573	A2591573 1M0401E15	C 325	12.8	13.8	47	17	AL024257	AL024257 oy14b08.x
C 253	13	14.0	45	17	BH805322	BH805322 1008066C0	C 326	12.8	13.8	49	9	AI208610	AI208610 g945h02.x
C 254	13	14.0	45	17	AL758853	AL758853 Arabidops	C 327	12.8	13.8	49	9	AA143103	AA143103 z669d05.x
C 255	13	14.0	46	10	AAV834537	AAV834537 Arabidops	C 328	12.8	13.8	49	9	AI1545773	AI1545773 fb65b02.y
C 256	13	14.0	46	17	AL768851	AL768851 Arabidops	C 329	12.8	13.8	49	9	AI1545773	AI1545773 fb65b02.y
C 257	13	14.0	46	17	CNS07F01	CNS07F01	C 330	12.8	13.8	49	9	AI1545773	AI1545773 fb65b02.y
C 258	13	14.0	47	14	TA9377	TA9377 ya74h03.s1	C 331	12.8	13.8	49	9	AA110762	AA110762 zc35e11.x
C 259	13	14.0	47	17	BH856706	BH856706 SALK_0793	C 332	12.8	13.8	49	13	BJ065777	BJ065777 BJ065777
C 260	13	14.0	48	9	AI384185	AI384185 fb17f03.y	C 333	12.8	13.8	49	14	C20874	C20874 HMG500494
C 261	13	14.0	48	17	A2385874	A2385874 1M0144M03	C 334	12.8	13.8	49	17	A2427327	A2427327 1M0209P11
C 262	13	14.0	48	17	A2385874	A2385874 1M0144M03	C 335	12.8	13.8	49	17	BH851976	BH851976 SALK_0738
C 263	13	14.0	48	17	HSCHO6F06	HSCHO6F06	C 336	12.8	13.8	50	9	AI0102898	AI0102898
C 264	13	14.0	48	17	TA1A0E08P	TA1A0E08P	C 337	12.8	13.8	50	9	AI0103452	AI0103452
C 265	13	14.0	48	17	TA1A0E08P	TA1A0E08P	C 338	12.8	13.8	50	9	AI0106642	AI0106642
C 266	13	14.0	49	14	C00961	C00961 HMG5000331	C 339	12.8	13.8	50	9	AI0107903	AI0107903
C 267	13	14.0	49	17	A2303685	A2303685 1M0030M08	C 340	12.8	13.8	50	13	BM319246	BM319246 K170C02.y
C 268	13	14.0	50	9	AU102795	AU102795 AU102795	C 341	12.6	13.5	29	14	A2510254	A2510254 1M0554F10
C 269	13	14.0	50	9	AU102867	AU102867 AU102867	C 342	12.6	13.5	29	14	A2510254	A2510254 1M0554F10
C 270	13	14.0	50	9	AU103363	AU103363 AU103363	C 343	12.6	13.5	29	14	A2510254	A2510254 1M0554F10
C 271	13	14.0	50	9	AU105566	AU105566 AU105566	C 344	12.6	13.5	29	14	A2510254	A2510254 1M0554F10
C 272	13	14.0	50	9	AU105660	AU105660 AU105660	C 345	12.6	13.5	31	17	A2308439	A2308439 1M0011T20
C 273	13	14.0	50	9	AU106332	AU106332 AU106332	C 346	12.6	13.5	31	17	AI010161	AI010161
C 274	13	14.0	50	9	AU106598	AU106598 AU106598	C 347	12.6	13.5	31	17	A2424567	A2424567 1M0204B18
C 275	13	14.0	50	9	AU106880	AU106880 AU106880	C 348	12.6	13.5	35	17	A2481110	A2481110 1M0303C09
C 276	13	14.0	50	9	AU107181	AU107181 AU107181	C 349	12.6	13.5	36	14	NS0146	NS0146 yz12f02.s1
C 277	13	14.0	50	9	AU107438	AU107438 AU107438	C 350	12.6	13.5	36	17	A2459382	A2459382 1M0264I07
C 278	13	14.0	50	9	AU107903	AU107903 AU107903	C 351	12.6	13.5	36	17	BH811607	BH811607 SALK_0591
C 279	13	14.0	50	10	BH616279	BH616279 BH616279	C 352	12.6	13.5	36	17	BH854787	BH854787
C 280	13	14.0	50	13	BJ049271	BJ049271 BJ049271	C 353	12.6	13.5	37	9	AI017811	AI017811
C 281	13	14.0	50	17	A2364704	A2364704 1M0110P24	C 354	12.6	13.5	37	9	AU256793	AU256793
C 282	13	13.8	25	14	H93534	H93534 yv08g12.t1	C 355	12.6	13.5	37	17	A2478803	A2478803
C 283	13	13.8	32	13	BM397244	BM397244 s818c02.y	C 356	12.6	13.5	37	17	A2622057	A2622057 1M0455M08
C 284	13	13.8	32	13	BM397244	BM397244 s818c02.y	C 357	12.6	13.5	37	17	A2648874	A2648874 2M0150M02
C 285	13	13.8	33	9	AA766921	AA766921 oc88e11.s	C 358	12.6	13.5	38	10	AAV81854	AAV81854
C 286	13	13.8	34	17	A2448375	A2448375 1M0246F05	C 359	12.6	13.5	38	10	AAV81854	AAV81854
C 287	13	13.8	34	17	BJ034483	BJ034483 BJ034483	C 360	12.6	13.5	38	17	A2459577	A2459577 1M0082K15
C 288	13	13.8	35	14	N38850	N38850 yv80e11.t1	C 361	12.6	13.5	38	17	A2459577	A2459577 1M0082K15
C 289	13	13.8	35	14	N38850	N38850 yv80e11.t1	C 362	12.6	13.5	39	10	AAV83097	AAV83097
C 290	13	13.8	35	17	BH855826	BH855826 SALK_0844	C 363	12.6	13.5	40	14	W98495	W98495 mg13d12.t1
C 291	13	13.8	35	17	BH855826	BH855826 SALK_0844	C 364	12.6	13.5	41	17	A2309895	A2309895 1M0017J14
C 292	13	13.8	37	13	BM026952	BM026952 GIT000021	C 365	12.6	13.5	42	17	AQ073112	AQ073112 EP.31677
C 293	13	13.8	37	17	AA591849	AA591849 1M0402B13	C 366	12.6	13.5	42	17	A2823130	A2823130 2M0097A04
C 294	13	13.8	38	14	D21039	D21039 HMG502023	C 367	12.6	13.5	42	17	BH000535	BH000535 2M028B05
C 295	13	13.8	38	17	A2371497	A2371497 1M0122019	C 368	12.6	13.5	42	17	BH790172	BH790172 SALK_0546
C 296	13	13.8	38	17	A2614509	A2614509 1M0443C19	C 369	12.6	13.5	42	17	TA348G010	TA348G010
C 297	13	13.8	39	13	BI757961	BI757961 603030677	C 370	12.6	13.5	43	9	AA811939	AA811939 OD72h01.s
C 298	13	13.8	40	12	BM330536	BM330536 602430418	C 371	12.6	13.5	43	17	BH740846	BH740846 KG05224-3

372	12.6	13.5	44	14	T6778	TE4778 ycs3h10.r1	445	12.4	13.3	43	17	A6843614
C 373	12.6	13.5	44	17	AZ778327	AZ778327 2M0013016	C 446	12.4	13.3	43	17	BH856046
C 374	12.6	13.5	45	9	AA009110	AA009110 m952509.r	C 447	12.4	13.3	44	10	AV833798
C 375	12.6	13.5	46	9	AI958696	AI958696 fc95609.y	C 448	12.4	13.3	44	14	H44436
C 376	12.6	13.5	46	9	AA508836	AA508836 n121h01.s	C 449	12.4	13.3	44	17	AZ314839
377	12.6	13.5	46	10	AV859991	AV859991 AV859991	450	12.4	13.3	44	17	AZ343874
378	12.6	13.5	46	17	BH848315	BH848315 SALK_0677	451	12.4	13.3	44	17	AZ393428
379	12.6	13.5	46	17	BH848315	BH848315 SALK_0677	452	12.4	13.3	44	17	AZ823752
380	12.6	13.5	46	17	BH879856	BH879856 SALK_0973	453	12.4	13.3	44	17	TA767847
C 381	12.6	13.5	47	14	H82798	H82798 yq48d06.s1	454	12.4	13.3	45	14	TA92229
C 382	12.6	13.5	47	17	AZ785454	AZ785454 2M0029421	455	12.4	13.3	45	17	BH853312
C 383	12.6	13.5	48	10	AW059775	AW059775 LE4H01.Y9	456	12.4	13.3	46	9	AA905936
C 384	12.6	13.5	49	9	AI192332	AI192332 qc97903.x	C 457	12.4	13.3	46	9	AA531890
C 385	12.6	13.5	49	9	AI189496	AI189496 qc97305.x	458	12.4	13.3	46	9	AA531890
C 386	12.6	13.5	49	9	AA576898	AA576898 nm78410.s	459	12.4	13.3	46	10	AV833578
C 387	12.6	13.5	49	10	BE271113	BE271113 600943605	460	12.4	13.3	46	14	H68899
C 388	12.6	13.5	49	14	H55111	H55111 CHR220050.C	461	12.4	13.3	46	17	AZ627975
C 389	12.6	13.5	49	14	R82145	R82145 4A1 CHROMOS	C 462	12.4	13.3	46	17	AZ814194
C 390	12.6	13.5	49	17	AZ814214	AZ814214 2M0081N13	463	12.4	13.3	46	17	TA92229
391	12.6	13.5	49	17	TA92229	TA92229 T. Bruce1	C 464	12.4	13.3	46	17	TA92229
392	12.6	13.5	50	9	AI02537	AI02537 AI02537	C 465	12.4	13.3	47	10	AV851220
393	12.6	13.5	50	9	AI02541	AI02541 AI02541	C 466	12.4	13.3	47	10	AV851220
394	12.6	13.5	50	9	AI02547	AI02547 AI02547	C 467	12.4	13.3	47	13	BM398772
395	12.6	13.5	50	9	AI02853	AI02853 AI02853	C 468	12.4	13.3	47	13	BM398772
396	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 469	12.4	13.3	47	17	AZ759762
397	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 470	12.4	13.3	47	17	AZ759762
C 398	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 471	12.4	13.3	47	17	AZ759762
C 399	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 472	12.4	13.3	47	17	AZ759762
C 400	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 473	12.4	13.3	47	17	AZ759762
C 401	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 474	12.4	13.3	47	17	AZ759762
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C 403	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 476	12.4	13.3	48	10	AV851220
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C 405	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 478	12.4	13.3	48	17	BH864995
C 406	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 479	12.4	13.3	49	14	C20870
C 407	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 480	12.4	13.3	49	17	AZ80010
C 408	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 481	12.4	13.3	49	17	BH851958
C 409	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 482	12.4	13.3	50	9	AI02229
C 410	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 483	12.4	13.3	50	9	AI02229
C 411	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 484	12.4	13.3	50	9	AI02229
C 412	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 485	12.4	13.3	50	9	AI02229
C 413	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 486	12.4	13.3	50	9	AI02229
C 414	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 487	12.4	13.3	50	9	AI02229
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C 418	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 491	12.4	13.3	50	9	AI02229
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C 420	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 493	12.4	13.3	50	9	AI02229
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C 423	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 496	12.4	13.3	50	9	AI02229
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C 427	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 500	12.4	13.3	50	9	AI02229
C 428	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 501	12.4	13.3	50	9	AI02229
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C 431	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 504	12.4	13.3	50	9	AI02229
C 432	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 505	12.4	13.3	50	9	AI02229
C 433	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 506	12.4	13.3	50	9	AI02229
C 434	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 507	12.4	13.3	50	9	AI02229
C 435	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 508	12.4	13.3	50	9	AI02229
C 436	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 509	12.4	13.3	50	9	AI02229
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C 438	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 511	12.4	13.3	50	9	AI02229
C 439	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 512	12.4	13.3	50	9	AI02229
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C 443	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 516	12.4	13.3	50	9	AI02229
C 444	12.6	13.5	50	9	AI02857	AI02857 AI02857	C 517	12.4	13.3	50	9	AI02229

C 518	12.2	13.1	33	17	A2334282	A2334282 1M0063B08	C 591	12.2	13.1	49	9	AA573818	AA573818 ns08a03.s
C 519	12.2	13.1	33	17	A2481715	A2481715 1M0306111	C 592	12.2	13.1	49	10	AA086799	AA086799 gk070211.y
C 520	12.2	13.1	34	9	AT116017	AT116017 ue23h05.x	C 593	12.2	13.1	49	12	BG179823	BG179823 602329028
C 521	12.2	13.1	34	9	AT1765722	AT1765722 w183902.x	C 594	12.2	13.1	49	13	B1518984	B1518984 603062281
C 522	12.2	13.1	34	13	B0304722	B0304722 BU034722	C 595	12.2	13.1	49	13	BM068828	BM068828 1685110.y
C 523	12.2	13.1	34	17	BH864816	BH864816 SALK.0969	C 596	12.2	13.1	49	14	BQ100687	BQ100687 1122c04.x
C 524	12.2	13.1	35	17	A2309035	A2309035 1M0012K11	C 597	12.2	13.1	50	9	AA654692	AA654692 nt73c03.s
C 525	12.2	13.1	35	17	A2490762	A2490762 1M0323M21	C 598	12.2	13.1	50	9	AU102226	AU102226 AU102226
C 526	12.2	13.1	36	13	B1246232	B1246232 602958773	C 599	12.2	13.1	50	9	AU102227	AU102227 AU102227
C 527	12.2	13.1	37	9	AA922819	AA922819 cms4a11.s	C 600	12.2	13.1	50	9	AU102229	AU102229 AU102229
C 528	12.2	13.1	37	9	AT808605	AT808605 wf56d12.x	C 601	12.2	13.1	50	9	AU102232	AU102232 AU102232
C 529	12.2	13.1	37	17	AZ351733	AZ351733 1M0089K21	C 602	12.2	13.1	50	9	AU102234	AU102234 AU102234
C 530	12.2	13.1	37	17	AZ460879	AZ460879 1M0266022	C 603	12.2	13.1	50	9	AU102237	AU102237 AU102237
C 531	12.2	13.1	37	17	AT460544	AT460544 Arabidops	C 604	12.2	13.1	50	9	AU102290	AU102290 AU102290
C 532	12.2	13.1	38	13	BF137365	BF137365 601780736	C 605	12.2	13.1	50	9	AU102298	AU102298 AU102298
C 533	12.2	13.1	38	13	B0303625	B0303625 B0303625	C 606	12.2	13.1	50	9	AU102354	AU102354 AU102354
C 534	12.2	13.1	38	14	N55471	N55471 yv48g04.sl	C 607	12.2	13.1	50	9	AU102355	AU102355 AU102355
C 535	12.2	13.1	38	17	TA83H04Q	TA83H04Q T. brucei	C 608	12.2	13.1	50	9	AU102664	AU102664 AU102664
C 536	12.2	13.1	39	17	AZ376781	AZ376781 1M0130K16	C 609	12.2	13.1	50	9	AU102993	AU102993 AU102993
C 537	12.2	13.1	40	9	AA862574	AA862574 oh44d09.s	C 610	12.2	13.1	50	9	AU103411	AU103411 AU103411
C 538	12.2	13.1	40	14	N75510	N75510 za84b07.sl	C 611	12.2	13.1	50	9	AU103905	AU103905 AU103905
C 539	12.2	13.1	40	14	RI7398	RI7398 y903d05.sl	C 612	12.2	13.1	50	9	AU104145	AU104145 AU104145
C 540	12.2	13.1	40	17	A2941994	A2941994 2M0202A01	C 613	12.2	13.1	50	9	AU104424	AU104424 AU104424
C 541	12.2	13.1	41	13	B03049697	B03049697 B04049697	C 614	12.2	13.1	50	9	AU104696	AU104696 AU104696
C 542	12.2	13.1	41	14	H93873	H93873 yv08e06.sl	C 615	12.2	13.1	50	9	AU105462	AU105462 AU105462
C 543	12.2	13.1	41	14	N74492	N74492 za54f06.sl	C 616	12.2	13.1	50	9	AU105592	AU105592 AU105592
C 544	12.2	13.1	41	17	AZ461404	AZ461404 1M0267F13	C 617	12.2	13.1	50	9	AU105798	AU105798 AU105798
C 545	12.2	13.1	41	17	AZ789628	AZ789628 2M0037A09	C 618	12.2	13.1	50	9	AU105846	AU105846 AU105846
C 546	12.2	13.1	41	17	AZ688304	AZ688304 2M0179P14	C 619	12.2	13.1	50	9	AU105969	AU105969 AU105969
C 547	12.2	13.1	41	17	AL756826	AL756826 Arabidops	C 620	12.2	13.1	50	9	AU106334	AU106334 AU106334
C 548	12.2	13.1	41	17	TA40DD1Q	TA40DD1Q T. brucei	C 621	12.2	13.1	50	9	AU106945	AU106945 AU106945
C 549	12.2	13.1	42	17	AZ620762	AZ620762 2M0093K09	C 622	12.2	13.1	50	9	AU107278	AU107278 AU107278
C 550	12.2	13.1	42	17	AL762458	AL762458 Arabidops	C 623	12.2	13.1	50	9	AU107283	AU107283 AU107283
C 551	12.2	13.1	42	17	AL770919	AL770919 Arabidops	C 624	12.2	13.1	50	9	AU107353	AU107353 AU107353
C 552	12.2	13.1	43	12	AA633126	AA633126 ng43d02.s	C 625	12.2	13.1	50	9	AU107537	AU107537 AU107537
C 553	12.2	13.1	43	12	BF114596	BF114596 SMOVAFCAP	C 626	12.2	13.1	50	9	AU107744	AU107744 AU107744
C 554	12.2	13.1	43	17	AZ432623	AZ432623 1M0218D08	C 627	12.2	13.1	50	9	AU107850	AU107850 AU107850
C 555	12.2	13.1	43	17	AZ450479	AZ450479 1M0219B16	C 628	12.2	13.1	50	10	AA550299	AA550299 T0062G10-
C 556	12.2	13.1	43	17	AZ658528	AZ658528 1M0535C14	C 629	12.2	13.1	50	10	BE042337	BE042337 hk35f08.y
C 557	12.2	13.1	43	9	AZ778245	AZ778245 2M0013O22	C 630	12.2	13.1	50	14	C20868	C20868 HUMS000493
C 558	12.2	13.1	44	14	W66525	W66525 EST083 chlc	C 631	12.2	13.1	50	17	AZ592619	AZ592619 1M0403110
C 559	12.2	13.1	44	14	AZ674461	AZ674461 2M0188P06	C 632	12.2	13.1	50	17	AU152319	AU152319 Arabidops
C 560	12.2	13.1	44	17	BH790298	BH790298 SALK.0567	C 633	12.2	13.1	50	17	TA19E08P	TA19E08P T. brucei
C 561	12.2	13.1	44	17	DR7117S	DR7117S Danio rerio	C 634	12.2	13.1	50	17	AZ810923	AZ810923 2M0076116
C 562	12.2	13.1	45	10	AV832654	AV832654 AYR32654	C 635	12.2	13.1	21	17	AZ436685	AZ436685 1M0082H02
C 563	12.2	13.1	45	17	AZ508443	AZ508443 1M0330F07	C 636	12.2	12.9	25	17	BH146175	BH146175 BE02743-5
C 565	12.2	13.1	45	17	AZ513479	AZ513479 1M0359P21	C 637	12.2	12.9	26	17	AZ787019	AZ787019 2M0032B19
C 566	12.2	13.1	45	17	AZ605963	AZ605963 1M0427A12	C 638	12.2	12.9	27	17	AZ440727	AZ440727 1M0211119
C 567	12.2	13.1	45	17	AZ796865	AZ796865 2M0052117	C 639	12.2	12.9	28	17	AZ844008	AZ844008 2M0133G01
C 568	12.2	13.1	45	17	BH631591	BH631591 1007085F0	C 640	12.2	12.9	30	17	AZ602612	AZ602612 1M0421022
C 569	12.2	13.1	45	17	TA379D04Q	TA379D04Q T. brucei	C 641	12.2	12.9	30	17	AZ829526	AZ829526 2M0107E17
C 570	12.2	13.1	46	9	AA878878	AA878878 t68bh03.s	C 642	12.2	12.9	31	9	AA890609	AA890609 ak12901.s
C 571	12.2	13.1	46	9	AT631110	AT631110 ts63e01.x	C 643	12.2	12.9	31	17	AZ375956	AZ375956 1M0129A08
C 572	12.2	13.1	46	9	AT925403	AT925403 wo20g12.x	C 644	12.2	12.9	33	17	AZ826390	AZ826390 2M0102003
C 573	12.2	13.1	46	17	AZ366724	AZ366724 1M0116003	C 645	12.2	12.9	34	14	N30244	N30244 yw64f03.sl
C 574	12.2	13.1	46	17	AZ439005	AZ439005 1M0229I20	C 646	12.2	12.9	34	17	AZ812567	AZ812567 2M0079N14
C 575	12.2	13.1	46	17	AZ660484	AZ660484 1M0538P03	C 647	12.2	12.9	34	17	AT63106	AT63106 2M0079N14
C 576	12.2	13.1	46	17	AZ805411	AZ805411 2M0066K14	C 648	12.2	12.9	34	17	AT830790	AT830790 2M0070E21
C 577	12.2	13.1	47	14	U44157	U44157 EMU44157.As	C 649	12.2	12.9	35	17	TA331H03P	TA331H03P T. brucei
C 578	12.2	13.1	47	17	AZ75502	AZ75502 2M0007G22	C 650	12.2	12.9	36	17	AZ14238	AZ14238 1M0030N24
C 579	12.2	13.1	47	17	AZ845343	AZ845343 2M0145B07	C 651	12.2	12.9	36	17	AZ337321	AZ337321 1M0067N23
C 580	12.2	13.1	47	17	BH851920	BH851920 SALK.0737	C 652	12.2	12.9	36	17	AA911865	AA911865 og21b08.s
C 581	12.2	13.1	47	17	BH897386	BH897386 3526.1-7-	C 653	12.2	12.9	37	9	AA617076	AA617076 601299222
C 582	12.2	13.1	47	17	AT466124	AT466124 Arabidops	C 654	12.2	12.9	37	10	BE407893	BE407893 2M0073M12
C 583	12.2	13.1	47	17	TA122802P	TA122802P T. brucei	C 655	12.2	12.9	37	17	AA025901	AA025901 122Y0962
C 584	12.2	13.1	48	13	B0303625	B0303625 B0303625	C 656	12.2	12.9	38	17	AU239786	AU239786 AU239786
C 585	12.2	13.1	48	17	AZ462540	AZ462540 1M0271I06	C 657	12.2	12.9	39	12	BF032106	BF032106 601559696
C 586	12.2	13.1	48	17	AZ576656	AZ576656 AST-T14C0	C 658	12.2	12.9	39	14	C53677	C53677 yu11
C 587	12.2	13.1	48	17	AZ588335	AZ588335 1M0396K24	C 659	12.2	12.9	39	17	AZ582385	AZ582385 1M0374E14
C 588	12.2	13.1	49	9	AT173140	AT173140 vz78c03.r	C 660	12.2	12.9	39	17		
C 589	12.2	13.1	49	9	AT1361792	AT1361792 qz24e12.x	C 661	12.2	12.9	39	17		
C 590	12.2	13.1	49	9	AT1361792	AT1361792 qz24e12.x	C 662	12.2	12.9	39	17		

664	12	12.9	39	17	BH66517	BH66517 SALK.1014	c 737	12	12.9	49	17	AZ664916	AZ664916 1M0545N04
665	12	12.9	40	9	AA932036	AA932036 coo5508.s	c 738	12	12.9	48	17	BH866729	BH866729 1008075C1
666	12	12.9	40	9	AI073810	AI073810 oy99305.x	c 739	12	12.9	50	9	AU102286	AU102286 AU102286
667	12	12.9	40	9	AI154170	AI154170 ud78h1.f	c 740	12	12.9	50	9	AU102294	AU102294 AU102294
668	12	12.9	40	17	AZ312880	AZ312880 1M0029D03	c 741	12	12.9	50	9	AU102300	AU102300 AU102300
669	12	12.9	41	17	AZ802791	AZ802791 2M0061N15	c 742	12	12.9	50	9	AU102304	AU102304 AU102304
670	12	12.9	41	17	AZ802948	AZ802948 2M0072E20	c 743	12	12.9	50	9	AU102385	AU102385 AU102385
671	12	12.9	41	17	BH854520	BH854520 K602089-5	c 744	12	12.9	50	9	AU102410	AU102410 AU102410
672	12	12.9	42	17	AZ304942	AZ304942 1M0005103	c 745	12	12.9	50	9	AU102489	AU102489 AU102489
673	12	12.9	42	17	AZ999883	AZ999883 1M0338P02	c 746	12	12.9	50	9	AU102866	AU102866 AU102866
674	12	12.9	42	17	BH792101	BH792101 SALK.0626	c 747	12	12.9	50	9	AU103087	AU103087 AU103087
675	12	12.9	43	9	AI910779	AI910779 w41h10.x	c 748	12	12.9	50	9	AU103563	AU103563 AU103563
676	12	12.9	43	9	AI931104	AI931104 fc7904.y	c 749	12	12.9	50	9	AU104879	AU104879 AU104879
677	12	12.9	43	9	AL798167	AL798167 AL798167	c 750	12	12.9	50	9	AU104885	AU104885 AU104885
678	12	12.9	43	10	AA518020	AA518020 v118f06.x	c 751	12	12.9	50	9	AU104893	AU104893 AU104893
679	12	12.9	43	10	AA580174	AA580174 AV850174	c 752	12	12.9	50	9	AU105564	AU105564 AU105564
680	12	12.9	43	14	D67709	D67709 CELK0763F	c 753	12	12.9	50	9	AU105565	AU105565 AU105565
681	12	12.9	43	14	R85006	R85006 yoa0e08.r1	c 754	12	12.9	50	9	AU105567	AU105567 AU105567
682	12	12.9	43	14	W09084	W09084 ma06c08.r1	c 755	12	12.9	50	9	AU105568	AU105568 AU105568
683	12	12.9	43	17	BH789347	BH789347 SALK.0190	c 756	12	12.9	50	9	AU105570	AU105570 AU105570
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1000 11.6 12.5 39 17 AZ479867 AZ479867 1M0300H24

```

ALIGNMENTS

```

RESULT 1
AZ514417/c 49 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0361N06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0361N06 F. DNA sequence.
ACCESSION AZ514417
VERSION AZ514417.1 GI:10695733
KEYWORDS GSS.
SOURCE Mus mouse.
ORGANISM Mus musculus
Mammalia: Eutheria: Rodentia: Sciurognathu: Muridae: Murinae: Mus.
1 (bases 1 to 49)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH GENOME CENTER
UNIVERSITY OF UTAH

```

```

FEATURES
Source
1. 49
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361N06"
/clone_1b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-gold, T1-resistant, F-"
/notes="vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[9b]AF23072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-gold (Stratagene) cells
and selected for ampicillin resistance."

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BASE COUNT
10 a 13 c 12 g 14 t
ORIGIN

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```

Query Match 22.24; Score 20.6; DB 17; Length 49;
Best Local Similarity 74.34; Pred. No. 3.7e+03;
Matches 26; Conservative 0; Mismatches 9; Indels 0;

```

```

QY 59 ATGTGACGTGCGGCTCCGAAACATTGACGCG 93
DB 39 ATGTGACGTGACGACCCGAGAGAGATGATG 5

```

```

RESULT 2
AL758166 49 bp DNA linear GSS 18-JUN-2002
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-156004-01240,
DEFINITION genomic survey sequence.
ACCESSION AL758166
VERSION AL758166.1 GI:21496514
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsi.
1
Strizhov, N., Li, Y., Rosso, M., Velever, P., Dekker, K., Siedler, H.
and Weiss, R.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished

```

```

JOURNAL
REFERENCE 2
AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weiss, R.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

```


ACCESSION A2317115
VERSION A2317115.1 GI:10365586
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: E column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
1..46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0035E20"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD22ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (g14732141g14732972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 11 a 15 c 11 g 9 t
ORIGIN
Query Match 18.7%; Score 17.4; DB 17; Length 46;
Best Local Similarity 77.8%; Pred. No. 5.1e+04;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TGGAGACACTCCATTCCTGCTGGGTGA 31
||||| ||||||| ||||||| |||||||
Db 38 TGGGACAGTCCTCATTCGACTGGGAGA 12

RESULT 6
H46101 39 bp mRNA linear EST 31-JUL-1995
LOCUS
DEFINITION
Y017402.r1 Soares adult brain N25HB55Y Homo sapiens cDNA clone IMAGE:178179 5' similar to gb:U14531 60S RIBOSOMAL PROTEIN L9

ACCESSION (HUMAN); mRNA sequence.
VERSION H46101
KEYWORDS H46101.1 GI:922153
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens.
AUTHORS Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 39)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 881
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 881 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 1.
Location/Qualifiers
1..39
/organism="Homo sapiens"
/db_xref="GDB:3840375"
/db_xref="taxon:9606"
/clone="IMAGE:178179"
/clone_1lb="Soares adult brain N25HB55Y"
/sex="Male"
/dev_stage="55-year Old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: brain; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCCATCAATCAATCGAGCGCGCGCTTTTCTTTTCTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

BASE COUNT 14 a 10 c 6 g 9 t
ORIGIN
Query Match 18.1%; Score 16.8; DB 14; Length 39;
Best Local Similarity 75.0%; Pred. No. 7.8e+04;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 56 GGATGTGACTGTGCGGCTCCAGAAA 83
||||| ||||||| ||||||| |||||||
Db 12 GCATTCAGACTGTGACATTCAGAAA 39

RESULT 7
A0103467

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177

ORGANISM	
	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)
AUTHORS	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hatake, Y., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakai, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (3), 388-393 (2001)
MEDLINE	21270072
COMMENT	Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and

FEATURES a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers
 source 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEP00195"
 /note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT 2 a 18 c 17 g 13 t
 ORIGIN

Query Match 17.2%; Score 16; DB 9; Length 50;
 Best Local Similarity 62.5%; Pred. No. 1.7e+05;
 Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 38 CTTGGTTTCACACTATCGAATGCTGCGGCTCC 77
 ||||| | | | | | | | | | | | | | | | | |
 4 CTTGGGTCGCTGCTGCTGCTGCTGCTGCTGCTCC 43

RESULT 10
 AUI04835 50 bp mRNA linear EST 30-AUG-2001
 LOCUS
 DEFINITION HEP00432, mRNA sequence.
 ACCESSION AUI06004
 VERSION AUI06004
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)

TITLE
 JOURNAL
 MEDLINE
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEP0432"
 /note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT 2 a 18 c 16 g 14 t
 ORIGIN

Query Match 17.2%; Score 16; DB 9; Length 50;
 Best Local Similarity 62.5%; Pred. No. 1.7e+05;
 Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 38 CTTGGTTTCACACTATCGAATGCTGCGGCTCC 77
 ||||| | | | | | | | | | | | | | | | | |
 4 CTTGGGTCGCTGCTGCTGCTGCTGCTGCTGCTCC 43

RESULT 11
 AUI04835 50 bp mRNA linear EST 30-AUG-2001
 LOCUS
 DEFINITION AUI04835 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ACCESSION HRC04434, mRNA sequence.
 AUI04835
 AUI04835.1 GI:13554356
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)

TITLE
 JOURNAL
 MEDLINE
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HRC0434"
 /note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT 6 a 17 c 17 g 10 t
 ORIGIN

Query Match 17.0%; Score 15.8; DB 9; Length 50;
 Best Local Similarity 74.1%; Pred. No. 2e+05;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 16 CATTCTGCTGCTGCTGCTGCTGCTGCTGG 42
 | | | | | | | | | | | | | | | | | | | | |
 17 CCTCTGCTGCTGCTGCTGCTGCTGCTGCTGG 43

RESULT 12
 BH855636 50 bp DNA linear GSS 08-JUL-2002
 LOCUS
 DEFINITION SALK_084858.34.85 x Arabidopsis thaliana TMDA insertion lines
 Arabidopsis thaliana genomic clone SALK_084858.34.85.x, DNA sequence.

ACCESSION BH855636
 VERSION BH855636
 KEYWORDS
 SOURCE
 ORGANISM
 thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 50)
 Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrian, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J., and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (Signal)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckersalk@ucsd.edu

This is single pass sequence recovered from the left border of

FEATURES	Location/Qualifiers
source	1. .50

Query Match	17.0%;	Score 15.8;	DB 17;	Length 50;
Best Local Similarity	74.1%;	Pred. No. 2e+05;		
Matches 20; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

0y 14 TCCATTCTGCGTGGGTGACATGCCTT 40
 |||| | | ||||| | | |||
 Db 1 TCCAGATGGGTGGGTGCATTTCCTT 27

RESULT 13					
A1446161/c					
LOCUS	A1446161	43 bp	mRNA	1linear	EST 13-APR-1995
DEFINITION	t107093.x1 NC1 CGAP_Cas4 Homo sapiens cDNA clone IMAGE:2140853,				

ACCESSION	AI446161
VERSION	AI446161.1
KEYWORDS	GI.4293271
SOURCE	EST:
	human,

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
1 (bases 1 to 43)

TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGSC clone distribution information can be found through the I.M.A.G.E. Consortium/INL at: www.bio.linn.gov/bbfp/image/image.html

Trace considered overall poor quality
Insert Length: 2385 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence step: 1.

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source
1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2140852"
/clone_1b="NC1_CGAP_Gas4"
/lisue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/notice="Organ: stomach; Vector: PCWV-SF08F6; Site:1: SallI
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.69 kb. Life Technologies catalog #
11549-011"

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Query Match	16.88;	Score 15.6;	DB 9;	Length 43;
Best Local Similarity	63.28;	Pred. NO. 2.2e+05;		
Matches 24;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;

Qy 8 GAGACACCCAAATTCGCTGGGTGACAAATCCCTGGTTT 45
| | | | | | | | | | | | | | | | | | | | | |
Db 42 GGGGACCCCTTTTGCTGGGGGCGGGGGTTCCTTT 5

RESULT	14
AU107296	
LOCUS	50 bp mRNA linear EST 30-AUG-2001
DEFINITION	AU107296 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ACCESSION	AU107296
VERSION	AU107296.1
KEYWORDS	EST.
SOURCE	human.

REFERENCE
AUTHORS

Eukaryota; Metazoa: Chordata: Vertebrata, Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hatake,

TITLE	Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MENTING	33270075

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuka@med.s.u-tokyo.ac.jp

FEATURES
SOURCE 1
EO
Location/Qualifiers
szuzuki, Y., Ioshimoto-Nakagawa, K., Maeyama, K., Suyama, A. and Sugano,
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LNC0949"
/clone_1kb="Sugano Homo sapiens cDNA library"

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BASE COUNT	8 a	14 c	12 g	16 t	dimethylmaleate treated U937 cells"
ORIGIN					
Overall Match					15.9% (range 15.6 - 20.0) (mean 16.9)

Best Local Similarity 63.2%; Pred. No. 2.3e+05;
Matches 24; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
GC 37 CCGTGGTTCAACATCAATGCAATGCAATGCGAGGC 74

3 CCCTCCCTCCTGAGACGTGTAAGAAATATGTCTCCAGGCC 40

Accession	LOCUS	DEFINITION
BR850482	36 bp DNA	linear GSS 13-JUN-2002
SALK_071136.42.10.x	Arabidopsis thaliana TDNA insertion lines	
Arabidopsis thaliana genomic clone SALK_071136.42.10.x	DNA sequence.	
BR850487		
BR850482		

VERNON	DR050402.1	GI:21421353
KEYWORDS	GS.	
SOURCE	thale cress.	
ORGANISM	<i>Arabidopsis thaliana</i>	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eudicotyledons; Malvales; Brassicales; Brassicaceae; Arabidopsis	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;

REFERENCE Rosidae; eurousids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 36)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadlinab,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednits,L., Shim,P.,
Zimmerman,J., and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
FEATURES
Location/Qualifiers
Class: TDNA tagged
1..36
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_071336.42.10.x"
/note="PCR was performed on Arabidopsis thaliana lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 12 a 7 c 5 g 12 t
ORIGIN
Query Match 16.68; Score 15.4; DB 17; Length 36;
Best Local Similarity 76.08; Pred. No. 2.4e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 33 AATGCTGGTTCACACTATGCG 57
||| ||||| ||||| |||
Db 6 AATACCTGGTTAAACACTACAG 30
||| ||||| ||||| |||
RESULT 16
LOCUS HSMC37D09 43 bp DNA linear GSS 29-MAY-1997
DEFINITION H.sapiens DNA for trapped exon (ID HMC37D09), genomic survey
sequence.
ACCESSION X88097
KEYWORDS X88097.1 GI:1437955
SOURCE GSS.
ORGANISM Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Chen,H.M., Rossier,C., Chrast,R. and Antonarakis,S.E.
TITLE Cloning of trapped exons from human chromosome 21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 43)
AUTHORS Antonarakis,S.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CHU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
3 (bases 1 to 43)
REFERENCE Chen,H., Chrast,R., Rossier,C., Morris,M.A., Laliofti,M.D. and
Antonarakis,S.E.
TITLE Cloning of 559 potential exons of genes of human chromosome 21 by
exon trapping
JOURNAL Genome Res. 6 (8), 747-760 (1996)
MEDLINE 97011340
PUBMED 8858350

FEATURES Location/Qualifiers
source 1..43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
exon 1..43
/note="trapped exon"
BASE COUNT 8 a 14 c 9 g 7 t 5 others
ORIGIN
Query Match 16.68; Score 15.4; DB 17; Length 43;
Best Local Similarity 57.98; Pred. No. 2.6e+05;
Matches 22; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 55 CGGATGTGACTGTGCGCCCTCCAGAAACATTGAGT 92
||| ||||| ||| ||||| ||| |||||
Db 43 CTGAGATGACTCGGAGNCCTCAGANTNAGCGTGT 6
||| ||||| ||| ||||| ||| |||||
RESULT 17
LOCUS BE566921 45 bp mRNA linear EST 15-AUG-2000
DEFINITION 6013410471 NIH_MGC_53 Homo sapiens cDNA IMAGE:3683506 5',
mRNA sequence.
ACCESSION BE566921
VERSION BE566921.1 GI:9810641
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 45)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM368 row: m column: 11.
FEATURES Location/Qualifiers
source 1..45
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3683506"
/clone_id="NIH_MGC_53"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
Site:1: SfiI (ggccgcctggcc); Site:2: SfiI (ggccatattggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCCATTAAGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGACGCGCCGACATG-AT(30)BN-3'
(where B = A, C, G or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 20 a 12 c 9 g 4 t
ORIGIN
Query Match 16.68; Score 15.4; DB 10; Length 45;
Best Local Similarity 61.08; Pred. No. 2.6e+05;
Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 24 CTGGGACATGCGCTTGGTTCAACTACTAGCATGGA 64
||| ||||| ||| ||||| ||| |||||
Db 1 CAGCATACAGCCATGATTCACACAAAGCGCATGGA 41
||| ||||| ||| ||||| ||| |||||


```

/db_xref="taxon:3702"
/clone="BK-026P11-013737"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (11) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

```

BASE COUNT	16 a	5 c	10 g	11 t
ORIGIN				
Query Match	16.18;	Score 15;	DB 17;	Length 42;
Best Local Similarity	78.38;	Pred. No. 3.6e+05;		
Matches 18;	Conservative	0;	Mismatches 5;	Indels 0;
0y	13	CTCCATTCGCTGGGTGACAT	35	
Db	39	CTCCATTTTCCCTTTGTGACTAT	17	

RESULT 30			
AA872957			
LOCUS	49 bp	mrna	linear
DEFINITION	AA872957		EST 19-MAY-1996
	0h63901.s1	ncl_CGAP_k1d5 Homo sapiens cDNA clone IMAGE:1471728 3'	

ACCESSION	AA872957	
VERSION	AA872957.1	GI:2969079

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
REFERENCE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nlm.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can
 be found through the I.M.A.G.E. Consortium/INL at:
www.bio.lnl.gov/btpr/image/image.html

```

Trice considered overall poor quality
Insert Length: 400 Std Error: 0.00
Seq primer: -40m13 fwd. ER from Amersham
High quality sequence stop: 1.

```

FEATURES
SOURCE

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1471728"
/clone_1b="NCI CCRP K1d5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10b"
/notes="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AAGTCGAGAAATTCGGCGGCGCAATATGTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library

```

BASE COUNT	9 a	11 c	13 g	16 t
ORIGIN	constructed by Bento Soares and M. Fatima Bonaldo.			
Query Match	16.1%; Score 15; DB 9; Length 49;			
Best local Similarity	67.7%; Pred. No. 3, 8e-05;			
Matches	21; Conservative	0; Mismatches	10; Indels	0; Gaps
Oy	43	TTTCAACACTATCGGAGTGTGAGTGGGC	73	
Db	5	TTTCAATCCCGGGGAATCCGGTTCTCGGC	35	

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Department of Virology,
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yasukure@ims.u-tokyo.ac.jp
Susuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Suganuma, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

BASE COUNT	ORIGIN
12 a	16 c 12 g 10 t
"note-Differential display comparison of untreated and dimethylsulfoxide treated 0937 cells"	
/clone_11b="Sugano Homo sapiens cDNA library" /db_xref="taxon:9606" /organism="homo sapiens" /db_xref="taxon:9606"	

Query Match	16.1%	Score 15	DB 9	Length 50
Best Local Similarity	67.7%	Pred. No. 3.9e+5		
Matches	21	Conservative	0	Mismatches 10
				Indels 0
				Gaps 0
QY	32	CAATGCCCTTGCTTCAACACATCGGAATCT	62	
DB	46	CCATGCTTGGCTACACCGCTACTGGAAGCT	16	

RESULT	32
C20586/c	
LOCUS	HUGHS0003674 Human adult (K.Okubo) 30 bp mRNA linear EST 23-OCT-1996
DEFINITION	sequence.
ACCESSION	C20586
VERSION	C20586.1 GI:1621696
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.


```

/clone_lib="NCI CGAP Co9"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo (Soares4
)."
```

BASE COUNT 10 a 7 c 5 g 18 t

Query Match 15.9%; Score 14.8; DB 9; Length 40;
Best Local Similarity 64.7%; Pred. NO. 4.1e+05;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 53 ATCGAATGTCATCTGCGGCTCCGAAACAT 86
Db 36 ATGCAATGTCATCTGCAAGATCAACAAAGAT 3

RESULT 36
AT591257/c 43 bp mRNA linear EST 14-DEC-1999
LOCUS tt75c06.x1 NCI CGAP HSC3 Homo sapiens cDNA clone IMAGE:224602 3'
DEFINITION similar to TR:008808 008808 P140MDA.; mRNA sequence.
ACCESSION AT591257
VERSION AT591257.1 GI:4600305
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html

Trace considered overall poor quality
Insert Length: 403 Std Error: 0.00
Seq primer: -40up from G1bco
High quality sequence stop: 1
POLA-No.

FEATURES
source 1..43
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:224602"
/clone_lib="NCI CGAP HSC3"
/tissue_type="CD34+ T negative, patient with chronic
myelogenous leukemia"
/lab_host="DH10B"
/note="Organ: Bone marrow; Vector: pAMP1. mRNA made from
lymphoid tissue, cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified. CDNA Library Preparation: David B.
Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer
Research 56:5380-5383."

FEATURES
source 1..40
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1159776"

BASE COUNT 10 a 7 c 12 g 7 t

Query Match 15.9%; Score 14.8; DB 17; Length 36;
Best Local Similarity 73.1%; Pred. NO. 3.9e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 44 TTCACACTATCGAATGTGACTGTC 69
Db 1 TTCACACTGTGGGAAGTCACTGCC 26

RESULT 35
AA631276 40 bp mRNA linear EST 31-OCT-1997
LOCUS ng92c01.s1 NCI CGAP Co9 Homo sapiens cDNA clone IMAGE:1159776 3'
DEFINITION similar to TR:E23957 E23957 CHROMOSOME XIV READING FRAME ORF
YNI153C.; mRNA sequence.
ACCESSION AA631276
VERSION AA631276.1 GI:2553887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html

Trace considered overall poor quality
Insert Length: 639 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE 1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 50)
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatahara,Y., Ohta,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL MEDLINE COMMENT	EMBO Rep. 2 (5), 388-393 (2001)
FEATURES	Location/Qualifiers
source	1. .50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="COL10026" /clone_1lb="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylformamide treated U937 cells"
BASE COUNT	12 a 10 c 16 g 12 t
ORIGIN	
Query Match	15.7%; Score 14.6; DB 9; Length 50;
Best Local Similarity	69.0%; Pred. No. 5.4e+05;
Matches	20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db	3 GCGGAGACACTCCATTCGCTGGGATGA 31 7 GCTGGAAGCGTTCTTTTCCCTAGATGA 35
RESULT 45	
AA922477	40 bp mRNA linear EST 17-JUN-1998
LOCUS	om33f09.s1 NCI-CGAP.GC4 Homo sapiens cDNA clone IMAGE:151881 3'
DEFINITION	similar to SW-BHP_HUMAN Q00341 HIGH DENSITY LIPOPROTEIN BINDING PROTEIN ;, mRNA sequence.
ACCESSION	AA922477.1
VERSION	AA922477.1 GI:3065786
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 40)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	AA922477.1
JOURNAL COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: c9apbs-remail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmerit-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.1nl.gov/bdrr/image/image.html

Trace considered overall poor quality
Insert length: 815 Std Error: 0.00
Seq primer: ~40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES	
source	Location/Qualifiers 1..40 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1551881" /clone_lib="NCI_GAB_Kat" /tissue_type="Pooled germ cell tumors" /lab_host="DH10B" /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	6 a 12 c 12 g 10 t
ORIGIN	
Query Match	15.5%; Score 14.4; DB 9; Length 40;
Best local similarity	60.0%; Pred. No. 5.7e+05;
Matches	24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Oy	36 GCCTGGTTTCACACTATTCGATGTGCATCGGCCCT 75 Db 1 GTCTGGCTCCTCGCTCGGAGAGCATGTCACACT 40
RESULT 46	
AL758462/c	40 bp DNA linear GSS 19-JUN-2002
LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-158H06-013215.
DEFINITION	genomic survey sequence.
ACCESSION	AL758462
VERSION	AL758462.1 GI:21496810
KEYWORDS	GSS.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 Strizhov,N., Li,Y., Rosso,M., Vlahovec,P., Dekker,K., Saedler,H. and Weishaar,B. A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines Unpublished 2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished 3 (bases 1 to 40) Li,Y., Strizhov,N., Rosso,M. and Weishaar,B. Direct Submission Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer Zuechungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g05870. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics Program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ . Location/Qualifiers 1..40 /organism="Arabidopsis thaliana" /strain="Columbia 0" /db_xref="taxon:3702" /clone="GK-158H06-013215" /clone_lib="Arabidopsis thaliana T-DNA insertion lines" /note="PCR was performed on DNA from Arabidopsis thaliana
COMMENT	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	

/lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescemu (engineered from
 pBluescript backbone); Site_1: BamHI; Site_2: BglII;
 Rescemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescemu, go to the web
 site 'www.zmsh.hastate.edu' and follow the links for
 'Rescemu'. Grid K was grown at Molokai, Hawaii in winter
 2000-2001. DNA was extracted from leaf punches, double
 digested using BamHI and BglII, and ligated to form
 circular plasmids. DH10 cells were transformed and then
 screened on LB plates with ampicillin."

Qy	32	CANAGCCTTGTTGCAACACTATCGAATGTG	63
Db	34	CCAACCCTTCGGTTCACGAATCTCGAAACG	3
Query Match	15.5%	Score 14.4	DB 17
Best Local Similarity	65.6%	Pred. No. 6.3e-05	
Matches	21	Conservative	0; Mismatches 11; Indels 0; Gaps 0;

RESULT 52	LOCUS	DEFINITION	ACCSSION
AA674026/c	AA674026	50 bp mRNA linear	EST 26-NOV-1997
		vp70006.r1 Knowles Solter mouse blastocyst B3 Mus musculus cDNA	
		clone IMAGE:1082027 5' similar to gb:U13661 Mouse	
		elongation factor 1-alpha (mouse)., mRNA sequence.	
		AA674026	

ACCESSION	AA674026
VERSION	AA674026.1
KEYWORDS	GI:2647308
SOURCE	EST.
ORGANISM	house mouse.
	Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 50)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T.,
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE	JOURNAL	COMMENT
The WashU-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouse@wustl.wustl.edu
This clone is available royalty-free through ILTIL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:596323
Trace considered overall poor quality
High quality sequence stop: 1.
Location/Qualifiers
1. .50

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1..50
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/dbxref="taxon:10090"
/clone="IMAGE:1082027"
/clone_lib="Knoves Solter mouse blastocyst B3"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="MH10B"
/note="Organ: embryo; Vector: pSPORT; Site 1: NotI; Site 2: SalI; cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGGTCCACGCGTACCGTTTCTTTTCTTTT-3'. cDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life

```

Technologies). Two different size selections: B1 (larger inserts) and B3.¹¹

Query Match	15.5%	Score 14.6	DB %	Length 50;
Best local Similarity	65.6%	Pred. No. 6	je-05;	
Matches	21	Conservative	0; Mismatches	11; Indels
				Gaps
OY	16	CATTGCGCTGGAGGCATACCTTGCTTCA	47	
Dc	50	CCCTTCGAAGGTTTTCAGCATTTGTATCA	19	

RESULT 53					
AU102972/C					
LOCUS	50 bp	mRNA	linear	EST 30-AUG-2001	
DEFINITION	AU102972	Sugano Homo sapiens CDNA library Homo sapiens clone			
ACCESSION	CC108352	mRNA sequence.			
VERSION	AU102972.1	GI:1352493			

ORGANISM
Homo sapiens
Eukaryota, Metazoa: Chordata, Vertebrata; Euteleostomi:
Actinoptera, Cyprinodontiformes, Poeciliidae, Poecilia
Mammalia: Eutheria: Primates, Catarrhini, Hominoidea, Homo.
1 (baes 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hattori, Y.,

REFERENCE
1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sesse, J., Hatake, Y., Ota, T., Isegaki, R., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Tataka Suzuki

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszuzuki@ims.u-tokyo.ac.jp
Suzuki Y., Yoshitomo-Nakagawa K., Maruyama K., and Sugano
S. Construction and characterization of a full length-enriched
and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

FEATURES
Source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COL08352"
/clone_1b="Sugano Homo sapiens CDNA library"
/notes="Differential display comparison of untreated and
dimethylmethyltreated treated U937 cells"
BASE COUNT      8 a      12 c      16 g      14 t
ORIGIN

```

Query Match	15.5%	Score 14.4	DB 95	Length 50
Best local Similarity	75.0%	Pred. No. 6	je05	
Matches 18	Conservative 0	Mismatches 6	Indels 0	Gaps 0
Qy	11	CACTCATTTCGCTGGGTGACAA	34	
	1	1	1	
Db	46	CGCCACACAGCTGCTGGGTGACCA	23	

RESULT	54
AU103596/c	
LOCUS	50 bp mRNA linear EST 30-AUG-20
DEFINITION	AU103596 Suidae Homo sapiens cDNA library Homo sapiens cDNA clone
CAZ03627,	mRNA sequence.
ACCESSION	AU103596
VERSION	AU103596.1 GI:13553117
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;	

REFERENCE Mammalia: Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"

BASE COUNT

12 a 14 c 19 g 5 t

ORIGIN

Query Match 15.5%; Score 14.4; DB 9; Length 50;
Best Local Similarity 60.0%; Pred. No. 6.3e+05;
Matches 24; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

2 AGCTGGAGACACTTCCTGCTGCTGACATGCTTG 41
||||| | | | | | | | | | | | | | | | | | | | |
40 AGCTGATGCCCTGCTTCACGCCGGGTCCACGCCGCTG 1

RESULT 55
AU0103598/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU0103598 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COLF6124, mRNA sequence.
ACCESSION AU0103598
VERSION AU0103598.1 GI:13553119
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 50)

REFERENCE Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"

BASE COUNT 8 a 16 c 19 g 7 t
ORIGIN

Query Match 15.5%; Score 14.4; DB 9; Length 50;
Best Local Similarity 60.0%; Pred. No. 6.3e+05;
Matches 24; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

2 AGCTGGAGACACTTCCTGCTGCTGACATGCTTG 41
||||| | | | | | | | | | | | | | | | | | | | |
50 AGCTGATGCCCTGCTTCACGCCGGGTCCACGCCGCTG 11

RESULT 56
AU0106860/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU0106860 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COL03340, mRNA sequence.
ACCESSION AU0106860
VERSION AU0106860.1 GI:135536381
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 50)

REFERENCE Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"

BASE COUNT 7 a 10 c 11 g 22 t
ORIGIN

Query Match 15.5%; Score 14.4; DB 9; Length 50;
Best Local Similarity 93.8%; Pred. No. 6.3e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 TTTCGCTGCTGCTGAC 33
||| | | | | | | | | | | | | | | | | | | | |
49 TTTCGCTGCTGCTGAC 34

RESULT 57
AV836264 50 bp mRNA linear EST 22-JUN-2001
LOCUS AV836264 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION AV836264 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgaris seedling leaves second leaf stage Hordeum vulgare subsp.
vulgaris cDNA clone basd2001, mRNA sequence.
ACCESSION AV836264
VERSION AV836264.1 GI:14528353
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473211419b/AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 4 c 10 g 13 t

Query Match 15.3%; Score 14.2; DB 17; Length 32;
Best Local Similarity 70.4%; Pred. No. 6.1e+05;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 18 TTCTGCTGGGTGACAAATGCTTGGTT 44
|||||
1 TTCTGCTGGGTGACAAATGCTTGGTT 27

RESULT 60
BH814159 36 bp DNA linear GSS 02-MAY-2002
LOCUS SALK_065834 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SALK_065834, DNA sequence.
ACCESSION BH814159
VERSION BH814159.1 GI:20393445
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 36)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
A Sequence-indexed library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..36
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_065834"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 13 a 4 c 8 g 11 t

Query Match 15.3%; Score 14.2; DB 17; Length 36;
Best Local Similarity 70.4%; Pred. No. 6.5e+05;

Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 14 TCATATTCGCTGGGTGACAAATGCTT 40
|||||
10 TCATATTCGCTGGGTGACAAATGCTT 36

RESULT 61
AZ992335 37 bp DNA linear GSS 27-APR-2001
LOCUS 2M0276023 Mouse 10kb plasmid UNGC2M library Mus musculus genomic
DEFINITION Clone UNGC2M0276023 R, DNA sequence.
ACCESSION AZ992335
VERSION AZ992335.1 GI:13863562
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84142, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: 0 column: 23
Seq primer: CACACAGAAACAGCTATGAC
Class: Plasmid ends
High quality sequence stop: 37.

FEATURES
source Location/Qualifiers
1..37
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG2M0276023"
/clone_lib="mouse 10kb plasmid UNGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g1473211419b/AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 11 a 6 c 8 g 12 t

Query Match 15.3%; Score 14.2; DB 17; Length 37;
Best Local Similarity 62.9%; Pred. No. 6.5e+05;

Query Match 15.3%; Score 14.2; DB 14; Length 40;
 Best Local Similarity 70.4%; Pred. No. 6.8e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2 AGCTGGAGACATTCCTGCGTGG 28
 ||||| ||||| ||||| ||||| |||||
 DB 34 AGATGGGCGCACCTCCTACCTCGG 8

RESULT 64
 A2663145 40 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0542D09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 DEFINITION clone UUGCIM0542D09 R. DNA sequence.

ACCESSION A2663145
 VERSION A2663145.1 GI:11800291
 KEYWORDS GSS.

ORGANISM

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meene, E., Pedersen, T., Kelly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,
 and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

CONTACT: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0542 row: D column: 09
 Seq primer: CACACAGCAACACGTCATACCC
 Class: plasmid ends
 High quality sequence stop: 40.
 Location/Qualifiers
 1..40
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0542D09"
 /clone_1fb="Mouse 10kb plasmid UUGCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nr; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1473214|9b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance.

BASE COUNT 13 a 6 c 10 g 11 t
 ORIGIN

Query Match 15.3%; Score 14.2; DB 17; Length 40;
 Best Local Similarity 62.9%; Pred. No. 6.8e+05;
 Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 52 TATCGAATGTGACTGCGGCTTCGAGAAACAT 86
 ||||| ||||| ||||| ||||| |||||
 DB 38 TATCGAATGTGACTGCGGCTTCGAGAAACAT 4

RESULT 65
 TA203E07P 41 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 203e07, forward sequence.
 DEFINITION genomic survey sequence.

ACCESSION AL476863
 VERSION AL476863.1 GI:11843427
 KEYWORDS GSS.

ORGANISM

Trypanosoma brucei.
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 41)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridgeshire CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

Constructured at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaidin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T-brucei/.

Location/Qualifiers
 1..41
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="203e07"

BASE COUNT 7 a 12 c 3 g 19 t
 ORIGIN

Query Match 15.3%; Score 14.2; DB 17; Length 41;
 Best Local Similarity 70.4%; Pred. No. 6.8e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 21 TGCCTGGGTGACAAATGCTTGGTTCA 47
 ||||| ||||| ||||| ||||| |||||
 DB 5 TGCCTGGGTGACAAATGCTTGGTTCA 31

RESULT 66
 BH890613C 45 bp DNA linear GSS 14-AUG-2002
 LOCUS BH890613 3526..1..4..1..G03..1EF..X..1 3526 - Rescued G1d K Zea mays genomic,
 DEFINITION DNA sequence.

ACCESSION BH890613
 VERSION BH890613.1 GI:2221585
 KEYWORDS GSS.

ORGANISM

Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

ACCESSION	HEP18556, mRNA sequence.
VERSION	AU104251
KEYWORDS	AU104251.1 GI:13553772
SOURCE	EST.
ORGANISM	human.
TITLE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)
REFERENCE	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata 'H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL	212/0072
MEDLINE	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano, 'S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
COMMENT	Location/Qualifiers 1..50 /organism="Homo sapiens" /DB_xref=taxon:9606" /clone="HEP18556" /clone_1lb="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylflumare treated U937 cells"
BASE COUNT	10 a 14 c 15 g 11 t
ORIGIN	
Best local Match	15.3%; Score 14.2; DB 9; Length 50;
Query Similarity	62.9%; Pred. No. 7.5e+05;
Matches	22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Oy	4 CTGGAGCACTCATTCTGCCGCGGTATGCATATGCC 38 13 CTGGCGTCCCGCATCTACTCTTGCGTAACGGGC 47
RESULT 70	
AU106145/c	50 bp mRNA linear EST 30-AUG-2001
LOCUS	AU106145 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION	HR006126, mRNA sequence.
ACCESSION	AU106145
VERSION	AU106145.1 GI:13555666
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)
REFERENCE	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata 'H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL	212/0072
MEDLINE	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano, 'S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
COMMENT	Location/Qualifiers
FEATURES	

source	1. 50	/organism="Homo sapiens"
	/db_xref="taxon:9606"	
	/clone="HRC06126"	
	/clone_lib="Sugano Homo sapiens cDNA library"	
	/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"	
BASE COUNT	10 a 21 c 10 g 9 t	
ORIGIN		
Query Match	15.3%; Score 14.2; DB 9; Length 50;	
Best Local Similarity	70.4%; Pred. No. 7.5e+05;	
Matches	19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
Db	6 GGGAGCACTCATTCTGCTGGCTGATC 32	
	43 GGGAGATCCGATGCTGGGTGATGATC 17	
RESULT 71		
LOCUS	AU106589 50 bp mRNA linear EST 30-AUG-2001	
DEFINITION	AU106589 Homo sapiens cDNA library Homo sapiens cDNA clone	
ACCESSION	KAT00765, mRNA sequence.	
VERSION	AU106589	
KEYWORDS	AU106589.1 GI:13556110	
SOURCE	EST.	
ORGANISM	human.	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata	
	'H., Ota,T., Isogai,T., Tanaka,Y., Morishita,S., Okubo,K., Sakaki	
TITLE	Y., Nakamura,Y., Suyama,A. and Sugano,S.	
	Diverse transcriptional initiation revealed by fine, large-scale	
	mapping of mRNA start sites	
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	
MEDLINE	21270072	
COMMENT	Contact: Yutaka Suzuki	
	Department of Virology	
	Institute of Medical Science, University of Tokyo	
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan	
	Email: yusuzuki@ims.u-tokyo.ac.jp	
	Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.	
	Construction and characterization of a full length-enriched and	
	a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
FEATURES	Location/Qualifiers	
source	1..50	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="KAT00765"	
	/clone_lib="Sugano Homo sapiens cDNA library"	
	/note="Differential display comparison of untreated and	
	dimethylflumarate treated U937 cells"	
BASE COUNT	7 a 17 c 17 g 9 t	
ORIGIN		
Query Match	15.3%; Score 14.2; DB 9; Length 50;	
Best Local Similarity	58.1%; Pred. No. 7.5e+05;	
Matches	25; Conservative 0; Mismatches 18; Indels 0; Gaps 0;	
Qy	16 CATCTGCTGGGCGACAAAGCTCTGTTCAACACTTTCGA 58	
	1 CTTTCCCTTGCTGCGAGCGCGAGAGCTGCAGAAAGCTCGA 43	
RESULT 72		
LOCUS	AZ443784 26 bp DNA linear GSS 04-OCT-2000	
DEFINITION	1M0238G02F Mouse 10kb plasmid UGCIM1 library Mus musculus genomic	
ACCESSION	clone UGCIM10238G02 F. DNA sequence.	
	AZ443784	

VERSION A2443784.1 GI:10592106
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinley, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0238 row: 6 column: 02
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1..26
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C1M0238602"
 /clone.lib="Mouse 10kb plasmid U06C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 6 c 7 g 9 t
 ORIGIN
 Query Match 15.1%; Score 14; DB 17; Length 26;
 Best Local Similarity 77.3%; Pred. No. 6.6e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 15 CCATTCTGCGCTGGTGACAAATG 36
 DB 4 CCATTCTGCGCTGGTGACAAATG 25

RESULT 73
 BM396571
 LOCUS
 DEFINITION 29 bp mRNA linear EST 17-JAN-2002
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM396571

VERSION BM396571.1 GI:18196609
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila.
 REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena. 1 (bases 1 to 29)
 AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Ortas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: 73.

BASE COUNT 6 a 8 c 11 g 3 t
 ORIGIN
 Query Match 15.1%; Score 14; DB 13; Length 29;
 Best Local Similarity 93.3%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCTGGAGCACTCC 16
 DB 6 AGCTGGAGCACTCC 20

RESULT 74
 A2484761 35 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0311024F Mouse 10kb plasmid U06C1M library Mus musculus genomic
 DEFINITION clone U06C1M0311024 F, DNA sequence.
 ACCESSION A2484761
 KEYWORDS A2484761.1 GI:10649916
 GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 35)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinley, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0311 row: 0 column: 24
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 35.

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DEFINITION AV852713 Nori Satoh unpublished CDNA library, egg Clona intestinalis CDNA clone rclcg22007 3', mRNA sequence.

ACCESSION AV852713

VERSION AV852713.1 GI:16838085

KEYWORDS EST.

SOURCE Clona intestinalis.

ORGANISM Clona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.

REFERENCE 1 (bases 1 to 39)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

TITLE Expressed genes in Clona intestinalis

JOURNAL Unpublished (2000)

COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidlan.zool.kyoto-u.ac.jp.

FEATURES
source
Location/Qualifiers
1..39
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="rclcg22007"
/clone_id="Nori Satoh unpublished CDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
/note="Vector: pBluescript SK"

BASE COUNT 11 a 8 c 9 g 10 t 1 others

ORIGIN

Query Match 15.1%; Score 14; DB 10; Length 39;
Best Local Similarity 66.7%; Pred. No. 7.9e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 58 AATGTCAGCTGCGGCTCCAGAAACATT 87
||||| | | | | | | | | | | | | | | | | | | | |
1 AATGTAAGTTGGCGCGACCAACCTT 30

DB 1 AATGTAAGTTGGCGCGACCAACCTT 30

RESULT 80

AZ501159 40 bp DNA linear GSS 05-OCT-2000

LOCUS IM0339H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC1M0339H19 R, DNA sequence.

ACCESSION AZ501159

VERSION AZ501159.1 GI:10682475

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0339 row: H column: 13
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends

FEATURES
source
Location/Qualifiers
1..40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0339H19"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473211419b) AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 8 c 4 g 11 t

ORIGIN

Query Match 15.1%; Score 14; DB 17; Length 40;
Best Local Similarity 60.5%; Pred. No. 8e+05;
Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 30 GACATGCTTGCTTACACATCGGATGCTACTG 67
||||| | | | | | | | | | | | | | | | | | | | |
1 GACATTCCTATGATTAACCTACACATATACAG 38

DB 1 GACATTCCTATGATTAACCTACACATATACAG 38

RESULT 81

AZ447897 43 bp DNA linear GSS 04-OCT-2000

LOCUS IM0245G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC1M0245G17 F, DNA sequence.

ACCESSION AZ447897

VERSION AZ447897.1 GI:10600152

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 43)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: G column: 17
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends


```

VERSION      AUI05649.1 GI:13555170
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL      Contact: Yutaka Suzuki
MEDLINE      Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
              ,S. Construction and characterization of a full length-enriched and
              a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HS102850"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT   10 a 13 c 21 g 6 t
ORIGIN
Query Match 15.1%; Score 14; DB 9; Length 50;
Best Local Similarity 66.7%; Pred. No. 8.8e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 36 GCGTGGTTTCACGACTGCGAATGTCGAC 65
|| ||| ||| ||| ||| ||| ||| |||
Db 42 GCACGGGCTCTACTACTACGCGATCGTGAC 13

RESULT 87
LOCUS       N85055 50 bp mRNA linear EST 01-APR-1996
DEFINITION J2084F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
N85055
ACCESSION   N85055.1 GI:1260680
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Llew C.C.
cdnas from fetal heart (1996)
unpublished (1996)
Contact: Llew C.C.
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cllw@rics.bwh.harvard.edu
Seq primer: GAATATTAACCTCATCAAGG.
FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="J2084"
/clone_lib="human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express. Site 1: EcoRI; Site 2:
XhoI. mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-0.1kg dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."
BASE COUNT   10 a 17 c 10 g 13 t
ORIGIN
Query Match 15.1%; Score 14; DB 14; Length 50;
Best Local Similarity 66.7%; Pred. No. 8.8e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 17 ATTTCGCTGCGTGCATGCTTGGTTTC 46
|| ||| ||| ||| ||| ||| ||| |||
Db 20 ATCTCTAGCGCGACTGATGATGTTGC 49

RESULT 88
LOCUS       A2580938/c 50 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0369A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0369A14 F, DNA sequence.
ACCESSION   A2580938
VERSION     A2580938.1 GI:11695451
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: A column: 14
Seq primer: CATTGTAAACGACGCGCCAGT
Class: Plasmid ends
High quality sequence stop: 50.
FEATURES
source
1..50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0369A14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, M1-resistant, F-."
/note="Vector: PMD42M; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number

```

Inducible derivative of plasmid pL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 12 c 10 g 18 t

ORIGIN

Query Match 15.18; Score 14; DB 17; Length 50;
Best Local Similarity 77.38; Pred. No. 8.6e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 48 ACACATCGCATGCTGCTC 69
||||| ||||| |||||
48 ACACAAATGATGATGCTGCTC 27

RESULT 89
BH789431 31 bp DNA linear GSS 02-APR-2002
LOCUS SALK_029414.47.75.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_029414.47.75.x, DNA sequence.

ACCESSION BH789431 GI:19882529
VERSION BH789431.1 GI:19882529
KEYWORDS GSS.

SOURCE

ORGANISM

thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

AUTHORS

Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadtrinh,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of Atlg17860 and 300 bases of the 3' end of Atlg17870.
Class: TDNA tagged.

FEATURES
Location/Qualifiers
1..31

/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"

/clone="SALK_029414.47.75.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 12 a 5 c 11 t

ORIGIN

Query Match 14.88; Score 13.8; DB 17; Length 31;
Best Local Similarity 72.08; Pred. No. 8.4e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 TGACAAATGCTTGTTCACACTA 53
||||| ||||| |||||
7 TTACAAATGCTTGTTCACACTA 31

DB

RESULT 90
DRL1H23T 33 bp DNA linear GSS 06-JUN-2002
LOCUS DRL1H23T
DEFINITION Dario rerio genomic clone Dkey-11H23, genomic survey sequence.
ACCESSION AL736291
VERSION AL736291.1 GI:21339656
KEYWORDS GSS.

SOURCE

zebrafish.

ORGANISM

Dario rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 33)
Humphray,S.J., Huckle,E. and Hunt,S.E.

AUTHORS

Submitted (06-JUN-2002)

JOURNAL

The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphray@sanger.ac.uk unpublished

COMMENT

This sequence was generated from the T7 end of BAC 11H23. 11H23 is part of the Dariokey Pilot BAC library created by R. Plasterk and N.V. Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

Location/Qualifiers
1..33

SOURCE

/organism="Dario rerio"
/db_xref="taxon:7955"

ORGANISM

/clone="Dkey-11H23"
/tissue-type="Testis"

REFERENCE

/note="vector pIndigoBAC-536"

BASE COUNT

7 a 12 c 7 g 7 t

ORIGIN

Query Match 14.88; Score 13.8; DB 17; Length 33;
Best Local Similarity 72.08; Pred. No. 8.6e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 34 ATGCTTGTTCACACTATCGGA 58
||||| ||||| |||||
25 ATGCTTGTTCACACTATCGGA 1

RESULT 91
AA048244/c 37 bp mRNA linear EST 09-SEP-1996
LOCUS mJ2/a04.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:47294 5' similar to SW:AS_XENLA P28824 A5 PROTEIN
PRECUSOR ; mRNA sequence.

ACCESSION

AA048244

VERSION

AA048244.1 GI:1527914

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 37)

JOURNAL

Marras,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

COMMENT

The WashU-HMI Mouse EST Project
Unpublished (1996)

JOURNAL

Contact: Maria M/Mouse EST Project

JOURNAL

WashU-HMI Mouse EST Project

JOURNAL

Washington University School of Medicine

JOURNAL

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

JOURNAL

Tel: 314 286 1800

JOURNAL

Fax: 314 286 1810

JOURNAL

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:288038

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. .37
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:477294"
/clone_1ib="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCAATCTGATAGTGGAGCGCGCGCAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 1]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
ORIGIN
9 a 12 c 9 g 7 t

Query Match 14.8%; Score 13.8; DB 9; Length 37;
Best Local Similarity 63.6%; Pred. No. 9.1e+05;
Matches 21; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GAGCTGGAGACACCTCATTCGCTGGTGACA 33
DB 34 GAGCTGGAGACACCTCATTCGCTGGTGACA 2

RESULT 92

A2317894/c

LOCUS

1M0036M13

DEFINITION

10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

A2317894

VERSION

A2317894.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus.

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 39)

Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.

and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000

Std Error: 0.00

Plate: 0036

row: M

column: 13

Seq primer: CACACGCAACACACTATGACC
Class: plasmid ends
High quality sequence stop: 39.

FEATURES

source

Location/Qualifiers
1. .39
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0036M13"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, 11-resistant, F-"
/note="vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (9114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
15 a 6 c 10 g 8 t

Query Match 14.8%; Score 13.8; DB 17; Length 39;
Best Local Similarity 72.0%; Pred. No. 9.3e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 21 TGCTGGGACACATCGCTTGT 45
DB 25 TTCTGTGTATCATCCCTGCTT 1

RESULT 93

AA642607

LOCUS

ng3n06.s1

DEFINITION

NCI-CGAP Pr22 Homo sapiens CDNA clone IMAGE:1158011 3'

similar to SW:CI0A.HUMAN P02745 COMPLEMENT C1Q SUBCOMPONENT, A

CHAIN PRECURSOR.; mRNA sequence.

AA642607

AA642607.1

GI:2567825

EST.

human.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 40)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaaps-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.lnl.gov/bdnp/image/image.html

Trace considered overall poor quality

Seq primer: -40M13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

QY 34 ATGCTTGGTTTCAACA 50
 |||||
 DB 11 ATGCTTGGTTGTCAGCA 27

RESULT 96
 LOCUS C00698/c 42 bp mRNA linear EST 23-JUL-1996
 DEFINITION HMW5008255 Human adult (K.Okubo) Homo sapiens CDNA, mRNA
 sequence.
 ACCESSION C00698
 VERSION C00698.1 GI:1432928
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Okubo, K.
 TITLE BodyMap: human gene expression database
 JOURNAL Unpublished (1995)
 COMMENT Contact: Okubo, K.
 Institute for Molecular and Cellular Biol
 Osaka University
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
 Tel: 06-877-5111(ex.3315)
 Email: kousaku@imcb.osaka-u.ac.jp
 Human Gene Signature, 3'-directed cDNA sequence. We are not
 submitting the same cDNA sequence redundantly to DDBJ since 1993.
 For the abundance information of clones with this sequence in this
 library and as well as in other 3'-directed libraries, see
 http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones
 represented by this GS sequences is also found there.

FEATURES
 source
 1..42
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Human adult (K.Okubo)"
 /dev_stage="adult"

/note="Organ: Blood; Vector: 1-qt-11; Site:1: Eco-RI;
 Monocytes were prepared from blood by ficoll-hypaque,
 percoll and T cell rosetting purification steps (purity:
 96%). mRNA was prepared from activated monocytes from a
 patient with rheumatoid arthritis. mRNA was reverse
 transcribed into 1-qt-11 vector. Using Eco-RI linkers cDNA was
 cloned into 1-qt-11 vector arms. The cDNA library was
 screened by differential hybridization using radioactively
 marked ss-cDNA from activated and non-activated
 monocytes.

BASE COUNT 9 a 9 c 7 g 15 t 2 others
 ORIGIN
 Query Match 14.8%; Score 13.8; DB 14; Length 42;
 Best Local Similarity 66.7%; Pred. No. 9.6e+05;
 Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 43 TTTCACACTATCGGAATGTGACTGTC 69
 ||| | | | | | | | | | | | | | | |
 DB 27 TTTTANCTATAGGAAGGAGGATGC 1

RESULT 97
 LOCUS BH643370 45 bp DNA linear GSS 14-FEB-2002
 DEFINITION 1008057C05.1BL_X1 1008 - Rescuemu Grid 1 Zea mays genomic, DNA
 sequence.
 ACCESSION BH643370
 VERSION BH643370.1 GI:18672167
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 45)
 AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered Rescuemu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 723 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1008057 row: 11
 Class: transposon-tagged.

FEATURES
 source
 1..45
 Location/Qualifiers
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_lib="1008 - Rescuemu Grid 1"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"

/note="Organ: leaf; Vector: Rescuemu (engineered from
 plasmid backbones); Site:1: BamHI; Site:2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescuemu, go to the web
 site 'Rescuemu.' Grid 1 was grown at Berkeley in 2001. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

BASE COUNT 4 a 17 c 15 g 9 t
 ORIGIN
 Query Match 14.8%; Score 13.8; DB 17; Length 45;
 Best Local Similarity 72.0%; Pred. No. 9.9e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 TGGGACACTCCATTCGCTGGGT 29
 | | | | | | | | | | | | | | | | | |
 DB 2 TAGCGGTGACGAGTTCGCTGGGT 26

RESULT 98
 LOCUS AM247861/c 48 bp mRNA linear EST 07-JAN-2000
 DEFINITION 2820451.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2820451 3',
 mRNA sequence.
 ACCESSION AM247861
 VERSION AM247861.1 GI:6590854
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 48)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2820451.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cga@pds-remail.nih.gov
 Tissue Procurement: DCTD/DRP CDNA Library Preparation: Ling
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (ILN) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can


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/db_xref="taxon:9606"
/clone="IMAGE:1505118"
/lab_host="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled: Vector: pT7n3D-Pac (Pharmacia) with
a modified polylinker: Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCL-GAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      12 a      14 c      4 g      19 t
ORIGIN

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Query Match      14.8%; Score 13.8; DB 9; Length 49;
Best Local Similarity 63.6%; Pred. No. 1e+06;
Matches 21; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY      56 GGAATGTGACTGTGGGCTTCGAGAAACATTG 88
      ||||| ||| | | | | | | | | |
Db      33 GGAATAAAGTGTGTGTCTCGAAGAGACATTG 1

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Search completed: July 5, 2003, 13:09:21
Job time : 1409 secs

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